SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PHOSPHOENOLPYRUVATE:SUGAR PHOSPHOTRANSFERASE SYSTEM PROTEINS
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<223> RXS00315

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ccg agc ttg gtg aac ggc tac gac gtg gcc gcc acc atg gct gcg ggc 163
Pro Ser Leu Val Asn Gly Tyr Asp Val Ala Ala Thr Met Ala Ala Gly
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gaa atg cca atg tgg tcc ctg ttt ggt tta gat gtt gcc caa gcc ggt 211
Glu Met Pro Met Trp Ser Leu Phe Gly Leu Asp Val Ala Gln Ala Gly
25 30 35

tac cag ggc acc gtg ctt cct gtg ctg gtg gtt tct tgg att ctg gca 259
Tyr Gln Gly Thr Val Leu Pro Val Leu Val Val Ser Trp Ile Leu Ala
40 45 50

acg atc gag aag ttc ctg cac aag cga ctc aag ggc act gca gac ttc 307
Thr Ile Glu Lys Phe Leu His Lys Arg Leu Lys Gly Thr Ala Asp Phe
55 60 65

ctg atc act cca gtg ctg acg ttg ctg ctc acc gga ttc ctt aca ttc 355
Leu Ile Thr Pro Val Leu Thr Leu Leu Leu Thr Gly Phe Leu Thr Phe
70 75 80 85

atc gcc att ggc cca gca atg cgc tgg gtg ggc gat gtg ctg gca cac 403
Ile Ala Ile Gly Pro Ala Met Arg Trp Val Gly Asp Val Leu Ala His
90 95 100

ggt cta cag gga ctt tat gat ttc ggt ggt cca gtc ggc ggt ctg ctc 451
Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly Pro Val Gly Gly Leu Leu
105 110 115

ttc ggt ctg gtc tac tca cca atc gtc atc act ggt ctg cac cag tcc 499

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Phe Gly Leu Val Tyr Ser Pro Ile Val Ile Thr Gly Leu His Gln Ser
        120                 125                 130

ttc ccg cca att gag ctg gag ctg ttt aac cag ggt gga tcc ttc atc   547
Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn Gln Gly Gly Ser Phe Ile
    135                 140                 145

ttc gca acg gca tct atg gct aat atc gcc cag ggt gcg gca tgt ttg   595
Phe Ala Thr Ala Ser Met Ala Asn Ile Ala Gln Gly Ala Ala Cys Leu
150                 155                 160                 165

gca gtg ttc ttc ctg gcg aag agt gaa aag ctc aag ggc ctt gca ggt   643
Ala Val Phe Phe Leu Ala Lys Ser Glu Lys Leu Lys Gly Leu Ala Gly
                170                 175                 180

gct tca ggt gtc tcc gct gtt ctt ggt att acg gag cct gcg atc ttc   691
Ala Ser Gly Val Ser Ala Val Leu Gly Ile Thr Glu Pro Ala Ile Phe
            185                 190                 195

ggt gtg aac ctt cgc ctg cgc tgg ccg ttc ttc atc ggt atc ggt acc   739
Gly Val Asn Leu Arg Leu Arg Trp Pro Phe Phe Ile Gly Ile Gly Thr
        200                 205                 210

gca gct atc ggt ggc gct ttg att gca ctc ttt aat atc aag gca gtt   787
Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu Phe Asn Ile Lys Ala Val
    215                 220                 225

gcg ttg ggc gct gca ggt ttc ttg ggt gtt gtt tct att gat gct cca   835
Ala Leu Gly Ala Ala Gly Phe Leu Gly Val Val Ser Ile Asp Ala Pro
230                 235                 240                 245

gat atg gtc atg ttc ttg gtg tgt gca gtt gtt acc ttc ttc atc gca   883
Asp Met Val Met Phe Leu Val Cys Ala Val Val Thr Phe Phe Ile Ala
                250                 255                 260

ttc ggc gca gcg att gct tat ggc ctt tac ttg gtt cgc cgc aac ggc   931
Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr Leu Val Arg Arg Asn Gly
            265                 270                 275

agc att gat cca gat gca acc gct gct cca gtg cct gca gga acg acc   979
Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro Val Pro Ala Gly Thr Thr
        280                 285                 290

aaa gcc gaa gca gaa gca ccc gca gaa ttt tca aac gat tcc acc atc
1027
Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe Ser Asn Asp Ser Thr Ile
    295                 300                 305

atc cag gca cct ttg acc ggt gaa gct att gca ctg agc agc gtc agc
1075
Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile Ala Leu Ser Ser Val Ser
310                 315                 320                 325

gat gcc atg ttt gcc agc gga aag ctt ggc tcg ggc gtt gcc atc gtc
1123
Asp Ala Met Phe Ala Ser Gly Lys Leu Gly Ser Gly Val Ala Ile Val
                330                 335                 340

cca acc aag ggg cag tta gtt tct ccg gtg agt gga aag att gtg gtg
1171
Pro Thr Lys Gly Gln Leu Val Ser Pro Val Ser Gly Lys Ile Val Val
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            345                 350                 355

gca ttc cca tct ggc cat gct ttc gca gtt cgc acc aag gct gag gat
1219
Ala Phe Pro Ser Gly His Ala Phe Ala Val Arg Thr Lys Ala Glu Asp
        360                 365                 370

ggt tcc aat gtg gat atc ttg atg cac att ggt ttc gac aca gta aac
1267
Gly Ser Asn Val Asp Ile Leu Met His Ile Gly Phe Asp Thr Val Asn
    375                 380                 385

ctc aac ggc acg cac ttt aac ccg ctg aag aag cag ggc gat gaa gtc
1315
Leu Asn Gly Thr His Phe Asn Pro Leu Lys Lys Gln Gly Asp Glu Val
390                 395                 400                 405

aaa gca ggg gag ctg ctg tgt gaa ttc gat att gat gcc att aag gct
1363
Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp Ile Asp Ala Ile Lys Ala
                410                 415                 420

gca ggt tat gag gta acc acg ccg att gtt gtt tcg aat tac aag aaa
1411
Ala Gly Tyr Glu Val Thr Thr Pro Ile Val Val Ser Asn Tyr Lys Lys
            425                 430                 435

acc gga cct gta aac act tac ggt ttg ggc gaa att gaa gcg gga gcc
1459
Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala
        440                 445                 450

aac ctg ctc aac gtc gca aag aaa gaa gcg gtg cca gca aca cca
1504
Asn Leu Leu Asn Val Ala Lys Lys Glu Ala Val Pro Ala Thr Pro
    455                 460                 465

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1527
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<400> 2

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Thr Met Ala Ala Gly Glu Met Pro Met Trp Ser Leu Phe Gly Leu Asp
             20                  25                  30

Val Ala Gln Ala Gly Tyr Gln Gly Thr Val Leu Pro Val Leu Val Val
         35                  40                  45

Ser Trp Ile Leu Ala Thr Ile Glu Lys Phe Leu His Lys Arg Leu Lys
     50                  55                  60

Gly Thr Ala Asp Phe Leu Ile Thr Pro Val Leu Thr Leu Leu Leu Thr
 65                  70                  75                  80
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Gly Phe Leu Thr Phe Ile Ala Ile Gly Pro Ala Met Arg Trp Val Gly
85 90 95

Asp Val Leu Ala His Gly Leu Gln Gly Leu Tyr Asp Phe Gly Gly Pro
100 105 110

Val Gly Gly Leu Leu Phe Gly Leu Val Tyr Ser Pro Ile Val Ile Thr
115 120 125

Gly Leu His Gln Ser Phe Pro Pro Ile Glu Leu Glu Leu Phe Asn Gln
130 135 140

Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser Met Ala Asn Ile Ala Gln
145 150 155 160

Gly Ala Ala Cys Leu Ala Val Phe Phe Leu Ala Lys Ser Glu Lys Leu
165 170 175

Lys Gly Leu Ala Gly Ala Ser Gly Val Ser Ala Val Leu Gly Ile Thr
180 185 190

Glu Pro Ala Ile Phe Gly Val Asn Leu Arg Leu Arg Trp Pro Phe Phe
195 200 205

Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly Ala Leu Ile Ala Leu Phe
210 215 220

Asn Ile Lys Ala Val Ala Leu Gly Ala Ala Gly Phe Leu Gly Val Val
225 230 235 240

Ser Ile Asp Ala Pro Asp Met Val Met Phe Leu Val Cys Ala Val Val
245 250 255

Thr Phe Phe Ile Ala Phe Gly Ala Ala Ile Ala Tyr Gly Leu Tyr Leu
260 265 270

Val Arg Arg Asn Gly Ser Ile Asp Pro Asp Ala Thr Ala Ala Pro Val
275 280 285

Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu Ala Pro Ala Glu Phe Ser
290 295 300

Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu Thr Gly Glu Ala Ile Ala
305 310 315 320

Leu Ser Ser Val Ser Asp Ala Met Phe Ala Ser Gly Lys Leu Gly Ser
325 330 335

Gly Val Ala Ile Val Pro Thr Lys Gly Gln Leu Val Ser Pro Val Ser
340 345 350

Gly Lys Ile Val Val Ala Phe Pro Ser Gly His Ala Phe Ala Val Arg
355 360 365

Thr Lys Ala Glu Asp Gly Ser Asn Val Asp Ile Leu Met His Ile Gly
370 375 380

Phe Asp Thr Val Asn Leu Asn Gly Thr His Phe Asn Pro Leu Lys Lys
385 390 395 400

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Gln Gly Asp Glu Val Lys Ala Gly Glu Leu Leu Cys Glu Phe Asp Ile
                405                 410                 415

Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val Thr Thr Pro Ile Val Val
            420                 425                 430

Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn Thr Tyr Gly Leu Gly Glu
        435                 440                 445

Ile Glu Ala Gly Ala Asn Leu Leu Asn Val Ala Lys Lys Glu Ala Val
    450                 455                 460

Pro Ala Thr Pro
465
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<223> FRXA00315

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Tyr Asp Phe Gly Gly Pro Val Gly Gly Leu Leu Phe Gly Leu Val Tyr
  1               5                  10                  15

tca cca atc gtc atc act ggt ctg cac cag tcc ttc ccg cca att gag   96
Ser Pro Ile Val Ile Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu
             20                  25                  30

ctg gag ctg ttt aac cag ggt gga tcc ttc atc ttc gca acg gca tct   144
Leu Glu Leu Phe Asn Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser
         35                  40                  45

atg gct aat atc gcc cag ggt gcg gca tgt ttg gca gtg ttc ttc ctg   192
Met Ala Asn Ile Ala Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu
     50                  55                  60

gcg aag agt gaa aag ctc aag ggc ctt gca ggt gct tca ggt gtc tcc   240
Ala Lys Ser Glu Lys Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser
 65                  70                  75                  80

gct gtt ctt ggt att acg gag cct gcg atc ttc ggt gtg aac ctt cgc   288
Ala Val Leu Gly Ile Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg
                 85                  90                  95

ctg cgc tgg ccg ttc ttc atc ggt atc ggt acc gca gct atc ggt ggc   336
Leu Arg Trp Pro Phe Phe Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly
            100                 105                 110

gct ttg att gca ctc ttt aat atc aag gca gtt gcg ttg ggc gct gca   384
Ala Leu Ile Ala Leu Phe Asn Ile Lys Ala Val Ala Leu Gly Ala Ala
        115                 120                 125

ggt ttc ttg ggt gtt gtt tct att gat gct cca gat atg gtc atg ttc   432
Gly Phe Leu Gly Val Val Ser Ile Asp Ala Pro Asp Met Val Met Phe
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    130                 135                 140

ttg gtg tgt gca gtt gtt acc ttc ttc atc gca ttc ggc gca gcg att    480
Leu Val Cys Ala Val Val Thr Phe Phe Ile Ala Phe Gly Ala Ala Ile
145                 150                 155                 160

gct tat ggc ctt tac ttg gtt cgc cgc aac ggc agc att gat cca gat    528
Ala Tyr Gly Leu Tyr Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp
                165                 170                 175

gca acc gct gct cca gtg cct gca gga acg acc aaa gcc gaa gca gaa    576
Ala Thr Ala Ala Pro Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu
            180                 185                 190

gca ccc gca gaa ttt tca aac gat tcc acc atc atc cag gca cct ttg    624
Ala Pro Ala Glu Phe Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu
        195                 200                 205

acc ggt gaa gct att gca ctg agc agc gtc agc gat gcc atg ttt gcc    672
Thr Gly Glu Ala Ile Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala
    210                 215                 220

agc gga aag ctt ggc tcg ggc gtt gcc atc gtc cca acc aag ggg cag    720
Ser Gly Lys Leu Gly Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln
225                 230                 235                 240

tta gtt tct ccg gtg agt gga aag att gtg gtg gca ttc cca tct ggc    768
Leu Val Ser Pro Val Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly
                245                 250                 255

cat gct ttc gca gtt cgc acc aag gct gag gat ggt tcc aat gtg gat    816
His Ala Phe Ala Val Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp
            260                 265                 270

atc ttg atg cac att ggt ttc gac aca gta aac ctc aac ggc acg cac    864
Ile Leu Met His Ile Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His
        275                 280                 285

ttt aac ccg ctg aag aag cag ggc gat gaa gtc aaa gca ggg gag ctg    912
Phe Asn Pro Leu Lys Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu
    290                 295                 300

ctg tgt gaa ttc gat att gat gcc att aag gct gca ggt tat gag gta    960
Leu Cys Glu Phe Asp Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val
305                 310                 315                 320

acc acg ccg att gtt gtt tcg aat tac aag aaa acc gga cct gta aac
1008
Thr Thr Pro Ile Val Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn
                325                 330                 335

act tac ggt ttg ggc gaa att gaa gcg gga gcc aac ctg ctc aac gtc
1056
Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val
            340                 345                 350

gca aag aaa gaa gcg gtg cca gca aca cca taagttgaaa ccttgagtgt
1106
Ala Lys Lys Glu Ala Val Pro Ala Thr Pro
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tcg
1109

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<213> Corynebacterium glutamicum

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Ser Pro Ile Val Ile Thr Gly Leu His Gln Ser Phe Pro Pro Ile Glu
             20                  25                  30

Leu Glu Leu Phe Asn Gln Gly Gly Ser Phe Ile Phe Ala Thr Ala Ser
         35                  40                  45

Met Ala Asn Ile Ala Gln Gly Ala Ala Cys Leu Ala Val Phe Phe Leu
     50                  55                  60

Ala Lys Ser Glu Lys Leu Lys Gly Leu Ala Gly Ala Ser Gly Val Ser
 65                  70                  75                  80

Ala Val Leu Gly Ile Thr Glu Pro Ala Ile Phe Gly Val Asn Leu Arg
                 85                  90                  95

Leu Arg Trp Pro Phe Phe Ile Gly Ile Gly Thr Ala Ala Ile Gly Gly
            100                 105                 110

Ala Leu Ile Ala Leu Phe Asn Ile Lys Ala Val Ala Leu Gly Ala Ala
        115                 120                 125

Gly Phe Leu Gly Val Val Ser Ile Asp Ala Pro Asp Met Val Met Phe
    130                 135                 140

Leu Val Cys Ala Val Val Thr Phe Phe Ile Ala Phe Gly Ala Ala Ile
145                 150                 155                 160

Ala Tyr Gly Leu Tyr Leu Val Arg Arg Asn Gly Ser Ile Asp Pro Asp
                165                 170                 175

Ala Thr Ala Ala Pro Val Pro Ala Gly Thr Thr Lys Ala Glu Ala Glu
            180                 185                 190

Ala Pro Ala Glu Phe Ser Asn Asp Ser Thr Ile Ile Gln Ala Pro Leu
        195                 200                 205

Thr Gly Glu Ala Ile Ala Leu Ser Ser Val Ser Asp Ala Met Phe Ala
    210                 215                 220

Ser Gly Lys Leu Gly Ser Gly Val Ala Ile Val Pro Thr Lys Gly Gln
225                 230                 235                 240

Leu Val Ser Pro Val Ser Gly Lys Ile Val Val Ala Phe Pro Ser Gly
                245                 250                 255

His Ala Phe Ala Val Arg Thr Lys Ala Glu Asp Gly Ser Asn Val Asp
            260                 265                 270
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Ile Leu Met His Ile Gly Phe Asp Thr Val Asn Leu Asn Gly Thr His
        275                 280                 285

Phe Asn Pro Leu Lys Lys Gln Gly Asp Glu Val Lys Ala Gly Glu Leu
    290                 295                 300

Leu Cys Glu Phe Asp Ile Asp Ala Ile Lys Ala Ala Gly Tyr Glu Val
305                 310                 315                 320

Thr Thr Pro Ile Val Val Ser Asn Tyr Lys Lys Thr Gly Pro Val Asn
                325                 330                 335

Thr Tyr Gly Leu Gly Glu Ile Glu Ala Gly Ala Asn Leu Leu Asn Val
            340                 345                 350

Ala Lys Lys Glu Ala Val Pro Ala Thr Pro
        355                 360


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cgacctatca aattctttat gctgcaggcg atgccttttc atg ttc ttg gca gtc   115
                                            Met Phe Leu Ala Val
                                              1               5

att ttg gcg att act gcg gct cgt aaa ttc ggt gcc aat gtc ttt aca   163
Ile Leu Ala Ile Thr Ala Ala Arg Lys Phe Gly Ala Asn Val Phe Thr
                10                  15                  20

tca gtc gca ctc gct ggt gca ttg ctg cac aca cag ctt cag gca gta   211
Ser Val Ala Leu Ala Gly Ala Leu Leu His Thr Gln Leu Gln Ala Val
            25                  30                  35

acc gtg ttg gtt gac ggt gaa ctc cag tcg atg act ctg gtg gct ttc   259
Thr Val Leu Val Asp Gly Glu Leu Gln Ser Met Thr Leu Val Ala Phe
        40                  45                  50

caa aag gct ggt aat gac gtc acc ttc ctg ggc att cca gtg gtg ctg   307
Gln Lys Ala Gly Asn Asp Val Thr Phe Leu Gly Ile Pro Val Val Leu
    55                  60                  65

cag ttg gcg ttg cat gta gcg agt ttg atg aag ttg tcg cga           349
Gln Leu Ala Leu His Val Ala Ser Leu Met Lys Leu Ser Arg
70                  75                  80

taagaggagg ggcgtgtcgg tct                                        372


<210> 6
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<212> PRT
<213> Corynebacterium glutamicum

<400> 6

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Met Phe Leu Ala Val Ile Leu Ala Ile Thr Ala Ala Arg Lys Phe Gly
  1               5                  10                  15

Ala Asn Val Phe Thr Ser Val Ala Leu Ala Gly Ala Leu Leu His Thr
             20                  25                  30

Gln Leu Gln Ala Val Thr Val Leu Val Asp Gly Glu Leu Gln Ser Met
         35                  40                  45

Thr Leu Val Ala Phe Gln Lys Ala Gly Asn Asp Val Thr Phe Leu Gly
     50                  55                  60

Ile Pro Val Val Leu Gln Leu Ala Leu His Val Ala Ser Leu Met Lys
 65                  70                  75                  80

Leu Ser Arg
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<223> RXN01299

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gtgcaacggt cacccaagtc aaaggattga aagaatcagc atg aat agc gta aat   115
                                            Met Asn Ser Val Asn
                                              1               5

aat tcc tcg ctt gtc cgg ctg gat gtc gat ttc ggc gac tcc acc acg   163
Asn Ser Ser Leu Val Arg Leu Asp Val Asp Phe Gly Asp Ser Thr Thr
                 10                  15                  20

gat gtc atc aac aac ctt gcc act gtt att ttc gac gct ggc cga gct   211
Asp Val Ile Asn Asn Leu Ala Thr Val Ile Phe Asp Ala Gly Arg Ala
             25                  30                  35

tcc tcc gcc gac gcc ctt gcc aaa gac gcg ctg gat cgt gaa gca aag   259
Ser Ser Ala Asp Ala Leu Ala Lys Asp Ala Leu Asp Arg Glu Ala Lys
         40                  45                  50

tcc ggc acc ggc gtt cct ggt caa gtt gct atc ccc cac tgc cgt tcc   307
Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile Pro His Cys Arg Ser
     55                  60                  65

gaa gcc gta tct gtc cct acc ttg ggc ttt gct cgc ctg agc aag ggt   355
Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala Arg Leu Ser Lys Gly
 70                  75                  80                  85

gtg gac ttc agc gga cct gat ggc gat gcc aac ttg gtg ttc ctc att   403
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Val Asp Phe Ser Gly Pro Asp Gly Asp Ala Asn Leu Val Phe Leu Ile
90 95 100

gca gca cct gct ggc ggc ggc aaa gag cac ctg aag atc ctg tcc aag 451
Ala Ala Pro Ala Gly Gly Gly Lys Glu His Leu Lys Ile Leu Ser Lys
105 110 115

ctt gct cgc tcc ttg gtg aag aag gat ttc atc aag gct ctg cag gaa 499
Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile Lys Ala Leu Gln Glu
120 125 130

gcc acc acc gag cag gaa atc gtc gac gtt gtc gat gcc gtg ctc aac 547
Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val Asp Ala Val Leu Asn
135 140 145

cca gca cca aaa acc acc gag cca gct gca gct ccg gct gcg gcg gcg 595
Pro Ala Pro Lys Thr Thr Glu Pro Ala Ala Ala Pro Ala Ala Ala Ala
150 155 160 165

gtt gct gag agt ggg gcg gcg tcg aca agc gtt act cgt atc gtg gca 643
Val Ala Glu Ser Gly Ala Ala Ser Thr Ser Val Thr Arg Ile Val Ala
170 175 180

atc acc gca tgc cca acc ggt atc gca cac acc tac atg gct gcg gat 691
Ile Thr Ala Cys Pro Thr Gly Ile Ala His Thr Tyr Met Ala Ala Asp
185 190 195

tcc ctg acg caa aac gcg gaa ggc cgc gat gat gtg gaa ctc gtt gtg 739
Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp Asp Val Glu Leu Val Val
200 205 210

gag act cag ggc tct tcc gct gtc acc cca gtc gat ccg aag atc atc 787
Glu Thr Gln Gly Ser Ser Ala Val Thr Pro Val Asp Pro Lys Ile Ile
215 220 225

gaa gct gcc gac gcc gtc atc ttc gcc acc gac gtg gga gtt aaa gac 835
Glu Ala Ala Asp Ala Val Ile Phe Ala Thr Asp Val Gly Val Lys Asp
230 235 240 245

cgc gag cgt ttc gct ggc aag cca gtc att gaa tcc ggc gtc aag cgc 883
Arg Glu Arg Phe Ala Gly Lys Pro Val Ile Glu Ser Gly Val Lys Arg
250 255 260

gcg atc aat gag cca gcc aag atg atc gac gag gcc atc gca gcc tcc 931
Ala Ile Asn Glu Pro Ala Lys Met Ile Asp Glu Ala Ile Ala Ala Ser
265 270 275

aag aac cca aac gcc cgc aag gtt tcc ggt tcc ggt gtc gcg gca tct 979
Lys Asn Pro Asn Ala Arg Lys Val Ser Gly Ser Gly Val Ala Ala Ser
280 285 290

gct gaa acc acc ggc gag aag ctc ggc tgg ggc aag cgc atc cag cag
1027
Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp Gly Lys Arg Ile Gln Gln
295 300 305

gca gtc atg acc ggc gtg tcc tac atg gtt cca ttc gta gct gcc ggc
1075
Ala Val Met Thr Gly Val Ser Tyr Met Val Pro Phe Val Ala Ala Gly
310 315 320 325

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ggc ctc ctg ttg gct ctc ggc ttc gca ttc ggt gga tac gac atg gcg
1123
Gly Leu Leu Leu Ala Leu Gly Phe Ala Phe Gly Gly Tyr Asp Met Ala
                330                 335                 340

aac ggc tgg caa gca atc gcc acc cag ttc tct ctg acc aac ctg cca
1171
Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe Ser Leu Thr Asn Leu Pro
            345                 350                 355

ggc aac acc gtc gat gtt gac ggc gtg gcc atg acc ttc gag cgt tca
1219
Gly Asn Thr Val Asp Val Asp Gly Val Ala Met Thr Phe Glu Arg Ser
        360                 365                 370

ggc ttc ctg ttg tac ttc ggc gca gtc ctg ttc gcc acc ggc caa gca
1267
Gly Phe Leu Leu Tyr Phe Gly Ala Val Leu Phe Ala Thr Gly Gln Ala
    375                 380                 385

gcc atg ggc ttc atc gtg gca gcc ctg tct ggc tac acc gca tac gca
1315
Ala Met Gly Phe Ile Val Ala Ala Leu Ser Gly Tyr Thr Ala Tyr Ala
390                 395                 400                 405

ctt gct gga cgc cca ggc atc gcg ccg ggc ttc gtc ggt ggc gcc atc
1363
Leu Ala Gly Arg Pro Gly Ile Ala Pro Gly Phe Val Gly Gly Ala Ile
                410                 415                 420

tcc gtc acc atc ggc gct ggc ttc att ggt ggt ctg gtt acc ggt atc
1411
Ser Val Thr Ile Gly Ala Gly Phe Ile Gly Gly Leu Val Thr Gly Ile
            425                 430                 435

ttg gct ggt ctc att gcc ctg tgg att ggc tcc tgg aag gtg cca cgc
1459
Leu Ala Gly Leu Ile Ala Leu Trp Ile Gly Ser Trp Lys Val Pro Arg
        440                 445                 450

gtg gtg cag tca ctg atg cct gtg gtc atc atc ccg cta ctt acc tca
1507
Val Val Gln Ser Leu Met Pro Val Val Ile Ile Pro Leu Leu Thr Ser
    455                 460                 465

gtg gtt gtt ggt ctc gtc atg tac ctc ctg ctg ggt cgc cca ctc gca
1555
Val Val Val Gly Leu Val Met Tyr Leu Leu Leu Gly Arg Pro Leu Ala
470                 475                 480                 485

tcc atc atg act ggt ttg cag gac tgg cta tcg tca atg tcc gga agc
1603
Ser Ile Met Thr Gly Leu Gln Asp Trp Leu Ser Ser Met Ser Gly Ser
                490                 495                 500

tcc gcc atc ttg ctg ggt atc atc ttg ggc ctc atg atg tgt ttc gac
1651
Ser Ala Ile Leu Leu Gly Ile Ile Leu Gly Leu Met Met Cys Phe Asp
            505                 510                 515
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ctc ggc gga cca gta aac aag gca gcc tac ctc ttt ggt acc gca ggc
1699
Leu Gly Gly Pro Val Asn Lys Ala Ala Tyr Leu Phe Gly Thr Ala Gly
        520                 525                 530

ctg tct acc ggc gac caa gct tcc atg gaa atc atg gcc gcg atc atg
1747
Leu Ser Thr Gly Asp Gln Ala Ser Met Glu Ile Met Ala Ala Ile Met
    535                 540                 545

gca gct ggc atg gtc cca cca atc gcg ttg tcc att gct acc ctg ctg
1795
Ala Ala Gly Met Val Pro Pro Ile Ala Leu Ser Ile Ala Thr Leu Leu
550                 555                 560                 565

cgc aag aag ctg ttc acc cca gca gag caa gaa aac ggc aag tct tcc
1843
Arg Lys Lys Leu Phe Thr Pro Ala Glu Gln Glu Asn Gly Lys Ser Ser
                570                 575                 580

tgg ctg ctt ggc ctg gca ttc gtc tcc gaa ggt gcc atc cca ttc gcc
1891
Trp Leu Leu Gly Leu Ala Phe Val Ser Glu Gly Ala Ile Pro Phe Ala
            585                 590                 595

gca gct gac cca ttc cgt gtg atc cca gca atg atg gct ggc ggt gca
1939
Ala Ala Asp Pro Phe Arg Val Ile Pro Ala Met Met Ala Gly Gly Ala
        600                 605                 610

acc act ggt gca atc tcc atg gca ctg ggc gtc ggc tct cgg gct cca
1987
Thr Thr Gly Ala Ile Ser Met Ala Leu Gly Val Gly Ser Arg Ala Pro
    615                 620                 625

cac ggc ggt atc ttc gtg gtc tgg gca atc gaa cca tgg tgg ggc tgg
2035
His Gly Gly Ile Phe Val Val Trp Ala Ile Glu Pro Trp Trp Gly Trp
630                 635                 640                 645

ctc atc gca ctt gca gca ggc acc atc gtg tcc acc atc gtt gtc atc
2083
Leu Ile Ala Leu Ala Ala Gly Thr Ile Val Ser Thr Ile Val Val Ile
                650                 655                 660

gca ctg aag cag ttc tgg cca aac aag gcc gtc gct gca gaa gtc gcg
2131
Ala Leu Lys Gln Phe Trp Pro Asn Lys Ala Val Ala Ala Glu Val Ala
            665                 670                 675

aag caa gaa gca caa caa gca gct gta aac gca taatcggacc ttgacccgat
2184
Lys Gln Glu Ala Gln Gln Ala Ala Val Asn Ala
        680                 685

gtc
2187
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<210> 8
<211> 688

<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Met Asn Ser Val Asn Asn Ser Ser Leu Val Arg Leu Asp Val Asp Phe
  1               5                  10                  15

Gly Asp Ser Thr Thr Asp Val Ile Asn Asn Leu Ala Thr Val Ile Phe
             20                  25                  30

Asp Ala Gly Arg Ala Ser Ser Ala Asp Ala Leu Ala Lys Asp Ala Leu
         35                  40                  45

Asp Arg Glu Ala Lys Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile
     50                  55                  60

Pro His Cys Arg Ser Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala
 65                  70                  75                  80

Arg Leu Ser Lys Gly Val Asp Phe Ser Gly Pro Asp Gly Asp Ala Asn
                 85                  90                  95

Leu Val Phe Leu Ile Ala Ala Pro Ala Gly Gly Gly Lys Glu His Leu
            100                 105                 110

Lys Ile Leu Ser Lys Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile
        115                 120                 125

Lys Ala Leu Gln Glu Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val
    130                 135                 140

Asp Ala Val Leu Asn Pro Ala Pro Lys Thr Thr Glu Pro Ala Ala Ala
145                 150                 155                 160

Pro Ala Ala Ala Ala Val Ala Glu Ser Gly Ala Ala Ser Thr Ser Val
                165                 170                 175

Thr Arg Ile Val Ala Ile Thr Ala Cys Pro Thr Gly Ile Ala His Thr
            180                 185                 190

Tyr Met Ala Ala Asp Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp Asp
        195                 200                 205

Val Glu Leu Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro Val
    210                 215                 220

Asp Pro Lys Ile Ile Glu Ala Ala Asp Ala Val Ile Phe Ala Thr Asp
225                 230                 235                 240

Val Gly Val Lys Asp Arg Glu Arg Phe Ala Gly Lys Pro Val Ile Glu
                245                 250                 255

Ser Gly Val Lys Arg Ala Ile Asn Glu Pro Ala Lys Met Ile Asp Glu
            260                 265                 270

Ala Ile Ala Ala Ser Lys Asn Pro Asn Ala Arg Lys Val Ser Gly Ser
        275                 280                 285

Gly Val Ala Ala Ser Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp Gly
    290                 295                 300
```

Lys Arg Ile Gln Gln Ala Val Met Thr Gly Val Ser Tyr Met Val Pro
305 310 315 320

Phe Val Ala Ala Gly Gly Leu Leu Leu Ala Leu Gly Phe Ala Phe Gly
325 330 335

Gly Tyr Asp Met Ala Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe Ser
340 345 350

Leu Thr Asn Leu Pro Gly Asn Thr Val Asp Val Asp Gly Val Ala Met
355 360 365

Thr Phe Glu Arg Ser Gly Phe Leu Leu Tyr Phe Gly Ala Val Leu Phe
370 375 380

Ala Thr Gly Gln Ala Ala Met Gly Phe Ile Val Ala Ala Leu Ser Gly
385 390 395 400

Tyr Thr Ala Tyr Ala Leu Ala Gly Arg Pro Gly Ile Ala Pro Gly Phe
405 410 415

Val Gly Gly Ala Ile Ser Val Thr Ile Gly Ala Gly Phe Ile Gly Gly
420 425 430

Leu Val Thr Gly Ile Leu Ala Gly Leu Ile Ala Leu Trp Ile Gly Ser
435 440 445

Trp Lys Val Pro Arg Val Val Gln Ser Leu Met Pro Val Val Ile Ile
450 455 460

Pro Leu Leu Thr Ser Val Val Val Gly Leu Val Met Tyr Leu Leu Leu
465 470 475 480

Gly Arg Pro Leu Ala Ser Ile Met Thr Gly Leu Gln Asp Trp Leu Ser
485 490 495

Ser Met Ser Gly Ser Ser Ala Ile Leu Leu Gly Ile Ile Leu Gly Leu
500 505 510

Met Met Cys Phe Asp Leu Gly Gly Pro Val Asn Lys Ala Ala Tyr Leu
515 520 525

Phe Gly Thr Ala Gly Leu Ser Thr Gly Asp Gln Ala Ser Met Glu Ile
530 535 540

Met Ala Ala Ile Met Ala Ala Gly Met Val Pro Pro Ile Ala Leu Ser
545 550 555 560

Ile Ala Thr Leu Leu Arg Lys Lys Leu Phe Thr Pro Ala Glu Gln Glu
565 570 575

Asn Gly Lys Ser Ser Trp Leu Leu Gly Leu Ala Phe Val Ser Glu Gly
580 585 590

Ala Ile Pro Phe Ala Ala Ala Asp Pro Phe Arg Val Ile Pro Ala Met
595 600 605

Met Ala Gly Gly Ala Thr Thr Gly Ala Ile Ser Met Ala Leu Gly Val
610 615 620

Gly Ser Arg Ala Pro His Gly Gly Ile Phe Val Val Trp Ala Ile Glu

```
625                 630                 635                 640

Pro Trp Trp Gly Trp Leu Ile Ala Leu Ala Ala Gly Thr Ile Val Ser
                645                 650                 655

Thr Ile Val Val Ile Ala Leu Lys Gln Phe Trp Pro Asn Lys Ala Val
            660                 665                 670

Ala Ala Glu Val Ala Lys Gln Glu Ala Gln Gln Ala Ala Val Asn Ala
        675                 680                 685
```

<210> 9
<211> 464
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(441)
<223> FRXA01299

<400> 9

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atg gaa atc atg gcc gcg atc atg gca gct ggc atg gtc cca cca atc   48
Met Glu Ile Met Ala Ala Ile Met Ala Ala Gly Met Val Pro Pro Ile
  1               5                  10                  15

gcg ttg tcc att gct acc ctg ctg cgc aag aag ctg ttc acc cca gca   96
Ala Leu Ser Ile Ala Thr Leu Leu Arg Lys Lys Leu Phe Thr Pro Ala
            20                  25                  30

gag caa gaa aac ggc aag tct tcc tgg ctg ctt ggc ctg gca ttc gtc   144
Glu Gln Glu Asn Gly Lys Ser Ser Trp Leu Leu Gly Leu Ala Phe Val
        35                  40                  45

tcc gaa ggt gcc atc cca ttc gcc gca gct gac cca ttc cgt gtg atc   192
Ser Glu Gly Ala Ile Pro Phe Ala Ala Ala Asp Pro Phe Arg Val Ile
    50                  55                  60

cca gca atg atg gct ggc ggt gca acc act ggt gca atc tcc atg gca   240
Pro Ala Met Met Ala Gly Gly Ala Thr Thr Gly Ala Ile Ser Met Ala
65                  70                  75                  80

ctg ggc gtc ggc tct cgg gct cca cac ggc ggt atc ttc gtg gtc tgg   288
Leu Gly Val Gly Ser Arg Ala Pro His Gly Gly Ile Phe Val Val Trp
                85                  90                  95

gca atc gaa cca tgg tgg ggc tgg ctc atc gca ctt gca gca ggc acc   336
Ala Ile Glu Pro Trp Trp Gly Trp Leu Ile Ala Leu Ala Ala Gly Thr
            100                 105                 110

atc gtg tcc acc atc gtt gtc atc gca ctg aag cag ttc tgg cca aac   384
Ile Val Ser Thr Ile Val Val Ile Ala Leu Lys Gln Phe Trp Pro Asn
        115                 120                 125

aag gcc gtc gct gca gaa gtc gcg aag caa gaa gca caa caa gca gct   432
Lys Ala Val Ala Ala Glu Val Ala Lys Gln Glu Ala Gln Gln Ala Ala
    130                 135                 140
```

gta aac gca taatcggacc ttgacccgat gtc 464
Val Asn Ala
145

<210> 10
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 10
Met Glu Ile Met Ala Ala Ile Met Ala Ala Gly Met Val Pro Pro Ile
1 5 10 15

Ala Leu Ser Ile Ala Thr Leu Leu Arg Lys Lys Leu Phe Thr Pro Ala
20 25 30

Glu Gln Glu Asn Gly Lys Ser Ser Trp Leu Leu Gly Leu Ala Phe Val
35 40 45

Ser Glu Gly Ala Ile Pro Phe Ala Ala Ala Asp Pro Phe Arg Val Ile
50 55 60

Pro Ala Met Met Ala Gly Gly Ala Thr Thr Gly Ala Ile Ser Met Ala
65 70 75 80

Leu Gly Val Gly Ser Arg Ala Pro His Gly Gly Ile Phe Val Val Trp
85 90 95

Ala Ile Glu Pro Trp Trp Gly Trp Leu Ile Ala Leu Ala Ala Gly Thr
100 105 110

Ile Val Ser Thr Ile Val Val Ile Ala Leu Lys Gln Phe Trp Pro Asn
115 120 125

Lys Ala Val Ala Ala Glu Val Ala Lys Gln Glu Ala Gln Gln Ala Ala
130 135 140

Val Asn Ala
145

<210> 11
<211> 580
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(580)
<223> FRXA01883

<400> 11
cgactgcggc gtctcttcct ggcactacca ttcctcgtcc tgaccaactc gccacagctg 60

gtgcaacggt cacccaagtc aaaggattga aagaatcagc atg aat agc gta aat 115
Met Asn Ser Val Asn
1 5

aat tcc tcg ctt gtc cgg ctg gat gtc gat ttc ggc gac tcc acc acg 163

```
Asn Ser Ser Leu Val Arg Leu Asp Val Asp Phe Gly Asp Ser Thr Thr
                 10                  15                  20

gat gtc atc aac aac ctt gcc act gtt att ttc gac gct ggc cga gct   211
Asp Val Ile Asn Asn Leu Ala Thr Val Ile Phe Asp Ala Gly Arg Ala
             25                  30                  35

tcc tcc gcc gac gcc ctt gcc aaa gac gcg ctg gat cgt gaa gca aag   259
Ser Ser Ala Asp Ala Leu Ala Lys Asp Ala Leu Asp Arg Glu Ala Lys
         40                  45                  50

tcc ggc acc ggc gtt cct ggt caa gtt gct atc ccc cac tgc cgt tcc   307
Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile Pro His Cys Arg Ser
     55                  60                  65

gaa gcc gta tct gtc cct acc ttg ggc ttt gct cgc ctg agc aag ggt   355
Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala Arg Leu Ser Lys Gly
 70                  75                  80                  85

gtg gac ttc agc gga cct gat ggc gat gcc aac ttg gtg ttc ctc att   403
Val Asp Phe Ser Gly Pro Asp Gly Asp Ala Asn Leu Val Phe Leu Ile
                 90                  95                 100

gca gca cct gct ggc ggc ggc aaa gag cac ctg aag atc ctg tcc aag   451
Ala Ala Pro Ala Gly Gly Gly Lys Glu His Leu Lys Ile Leu Ser Lys
             105                 110                 115

ctt gct cgc tcc ttg gtg aag aag gat ttc atc aag gct ctg cag gaa   499
Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile Lys Ala Leu Gln Glu
         120                 125                 130

gcc acc acc gag cag gaa atc gtc gac gtt gtc gat gcc gtg ctc aac   547
Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val Asp Ala Val Leu Asn
     135                 140                 145

cca gca cca aaa aac cac cga gcc agc tgc agc                       580
Pro Ala Pro Lys Asn His Arg Ala Ser Cys Ser
150                 155                 160
```


<210> 12
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 12

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Met Asn Ser Val Asn Asn Ser Ser Leu Val Arg Leu Asp Val Asp Phe
  1               5                  10                  15

Gly Asp Ser Thr Thr Asp Val Ile Asn Asn Leu Ala Thr Val Ile Phe
             20                  25                  30

Asp Ala Gly Arg Ala Ser Ser Ala Asp Ala Leu Ala Lys Asp Ala Leu
         35                  40                  45

Asp Arg Glu Ala Lys Ser Gly Thr Gly Val Pro Gly Gln Val Ala Ile
     50                  55                  60

Pro His Cys Arg Ser Glu Ala Val Ser Val Pro Thr Leu Gly Phe Ala
 65                  70                  75                  80
```

```
Arg Leu Ser Lys Gly Val Asp Phe Ser Gly Pro Asp Gly Asp Ala Asn
                 85                  90                  95

Leu Val Phe Leu Ile Ala Ala Pro Ala Gly Gly Gly Lys Glu His Leu
            100                 105                 110

Lys Ile Leu Ser Lys Leu Ala Arg Ser Leu Val Lys Lys Asp Phe Ile
        115                 120                 125

Lys Ala Leu Gln Glu Ala Thr Thr Glu Gln Glu Ile Val Asp Val Val
    130                 135                 140

Asp Ala Val Leu Asn Pro Ala Pro Lys Asn His Arg Ala Ser Cys Ser
145                 150                 155                 160
```

<210> 13
<211> 631
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (77)..(631)
<223> FRXA01889

<400> 13

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accgagccag ctgcagctcc ggctgcggcg gccggttgtt aagagtgggg cggcgtcgac 60

aagcgttact cgtatcgtg gca atc acc gca tgc cca acc ggt atc gca cac  112
                 Val Ala Ile Thr Ala Cys Pro Thr Gly Ile Ala His
                   1               5                  10

acc tac atg gct gcg gat tcc ctg acg caa aac gcg gaa ggc cgc gat   160
Thr Tyr Met Ala Ala Asp Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp
         15                  20                  25

gat gtg gaa ctc gtt gtg gag act cag ggc tct tcc gct gtc acc cca   208
Asp Val Glu Leu Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro
     30                  35                  40

gtc gat ccg aag atc atc gaa gct gcc gac gcc gtc atc ttc gcc acc   256
Val Asp Pro Lys Ile Ile Glu Ala Ala Asp Ala Val Ile Phe Ala Thr
 45                  50                  55                  60

gac gtg gga gtt aaa gac cgc gag cgt ttc gct ggc aag cca gtc att   304
Asp Val Gly Val Lys Asp Arg Glu Arg Phe Ala Gly Lys Pro Val Ile
                 65                  70                  75

gaa tcc ggc gtc aag cgc gcg atc aat gag cca gcc aag atg atc gac   352
Glu Ser Gly Val Lys Arg Ala Ile Asn Glu Pro Ala Lys Met Ile Asp
             80                  85                  90

gag gcc atc gca gcc tcc aag aac cca aac gcc cgc aag gtt tcc ggt   400
Glu Ala Ile Ala Ala Ser Lys Asn Pro Asn Ala Arg Lys Val Ser Gly
         95                  100                 105

tcc ggt gtc gcg gca tct gct gaa acc acc ggc gag aag ctc ggc tgg   448
```

```
Ser Gly Val Ala Ala Ser Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp
    110                 115                 120

ggc aag cgc atc cag cag gca gtc atg acc ggc gtg tcc tac atg gtt   496
Gly Lys Arg Ile Gln Gln Ala Val Met Thr Gly Val Ser Tyr Met Val
125                 130                 135                 140

cca ttc gta gct gcc ggc ggc ctc ctg ttg gct ctc ggc ttc gca ttc   544
Pro Phe Val Ala Ala Gly Gly Leu Leu Leu Ala Leu Gly Phe Ala Phe
                145                 150                 155

ggt gga tac gac atg gcg aac ggc tgg caa gca atc gcc acc cag ttc   592
Gly Gly Tyr Asp Met Ala Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe
            160                 165                 170

tct ctg acc aac ctg cca ggc aac acc gtc gat gtt gac               631
Ser Leu Thr Asn Leu Pro Gly Asn Thr Val Asp Val Asp
        175                 180                 185


<210> 14
<211> 185
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Val Ala Ile Thr Ala Cys Pro Thr Gly Ile Ala His Thr Tyr Met Ala
  1               5                  10                  15

Ala Asp Ser Leu Thr Gln Asn Ala Glu Gly Arg Asp Asp Val Glu Leu
             20                  25                  30

Val Val Glu Thr Gln Gly Ser Ser Ala Val Thr Pro Val Asp Pro Lys
         35                  40                  45

Ile Ile Glu Ala Ala Asp Ala Val Ile Phe Ala Thr Asp Val Gly Val
     50                  55                  60

Lys Asp Arg Glu Arg Phe Ala Gly Lys Pro Val Ile Glu Ser Gly Val
 65                  70                  75                  80

Lys Arg Ala Ile Asn Glu Pro Ala Lys Met Ile Asp Glu Ala Ile Ala
                 85                  90                  95

Ala Ser Lys Asn Pro Asn Ala Arg Lys Val Ser Gly Ser Gly Val Ala
            100                 105                 110

Ala Ser Ala Glu Thr Thr Gly Glu Lys Leu Gly Trp Gly Lys Arg Ile
        115                 120                 125

Gln Gln Ala Val Met Thr Gly Val Ser Tyr Met Val Pro Phe Val Ala
    130                 135                 140

Ala Gly Gly Leu Leu Leu Ala Leu Gly Phe Ala Phe Gly Gly Tyr Asp
145                 150                 155                 160

Met Ala Asn Gly Trp Gln Ala Ile Ala Thr Gln Phe Ser Leu Thr Asn
                165                 170                 175

Leu Pro Gly Asn Thr Val Asp Val Asp
            180                 185
```

<210> 15
<211> 416
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(393)
<223> RXA00951

<400> 15

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atc caa gca atc tta gag aag gca gca gcg ccg gcg aag cag aag gct   48
Ile Gln Ala Ile Leu Glu Lys Ala Ala Ala Pro Ala Lys Gln Lys Ala
  1               5                  10                  15

cct gct gtg gct cct gct gta aca ccc act gac gct cct gca gcc tca   96
Pro Ala Val Ala Pro Ala Val Thr Pro Thr Asp Ala Pro Ala Ala Ser
             20                  25                  30

gtc caa tcc aaa acc cac gac aag atc ctc acc gtc tgt ggc aac ggc  144
Val Gln Ser Lys Thr His Asp Lys Ile Leu Thr Val Cys Gly Asn Gly
         35                  40                  45

ttg ggt acc tcc ctc ttc ctc aaa aac acc ctt gag caa gtt ttc gac  192
Leu Gly Thr Ser Leu Phe Leu Lys Asn Thr Leu Glu Gln Val Phe Asp
     50                  55                  60

acc tgg ggt tgg ggt cca tac atg acg gtg gag gca acc gac act atc  240
Thr Trp Gly Trp Gly Pro Tyr Met Thr Val Glu Ala Thr Asp Thr Ile
 65                  70                  75                  80

tcc gcc aag ggc aaa gcc aag gaa gct gat ctc atc atg acc tct ggt  288
Ser Ala Lys Gly Lys Ala Lys Glu Ala Asp Leu Ile Met Thr Ser Gly
                 85                  90                  95

gaa atc gcc cgc acg ttg ggt gat gtt gga atc ccg gtt cac gtg atc  336
Glu Ile Ala Arg Thr Leu Gly Asp Val Gly Ile Pro Val His Val Ile
            100                 105                 110

aat gac ttc acg agc acc gat gaa atc gat gct gcg ctt cgt gaa cgc  384
Asn Asp Phe Thr Ser Thr Asp Glu Ile Asp Ala Ala Leu Arg Glu Arg
        115                 120                 125

tac gac atc taactacttt aaaaggacga aaa                           416
Tyr Asp Ile
    130
```

<210> 16
<211> 131
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

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Ile Gln Ala Ile Leu Glu Lys Ala Ala Ala Pro Ala Lys Gln Lys Ala
  1               5                  10                  15

Pro Ala Val Ala Pro Ala Val Thr Pro Thr Asp Ala Pro Ala Ala Ser
             20                  25                  30
```

Val Gln Ser Lys Thr His Asp Lys Ile Leu Thr Val Cys Gly Asn Gly
35 40 45

Leu Gly Thr Ser Leu Phe Leu Lys Asn Thr Leu Glu Gln Val Phe Asp
50 55 60

Thr Trp Gly Trp Gly Pro Tyr Met Thr Val Glu Ala Thr Asp Thr Ile
65 70 75 80

Ser Ala Lys Gly Lys Ala Lys Glu Ala Asp Leu Ile Met Thr Ser Gly
85 90 95

Glu Ile Ala Arg Thr Leu Gly Asp Val Gly Ile Pro Val His Val Ile
100 105 110

Asn Asp Phe Thr Ser Thr Asp Glu Ile Asp Ala Ala Leu Arg Glu Arg
115 120 125

Tyr Asp Ile
130

<210> 17
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> RXN01244

<400> 17
gatatgtgtt tgtttgtcaa tatccaaatg tttgaatagt tgcacaactg ttggttttgt 60

ggtgatcttg aggaaattaa ctcaatgatt gtgaggatgg gtg gct act gtg gct 115
Val Ala Thr Val Ala
1 5

gat gtg aat caa gac act gta ctg aag ggc acc ggc gtt gtc ggt gga 163
Asp Val Asn Gln Asp Thr Val Leu Lys Gly Thr Gly Val Val Gly Gly
10 15 20

gtc cgt tat gca agc gcg gtg tgg att acc cca cgc ccc gaa cta ccc 211
Val Arg Tyr Ala Ser Ala Val Trp Ile Thr Pro Arg Pro Glu Leu Pro
25 30 35

caa gca ggc gaa gtc gtc gcc gaa gaa aac cgt gaa gca gag cag gag 259
Gln Ala Gly Glu Val Val Ala Glu Glu Asn Arg Glu Ala Glu Gln Glu
40 45 50

cgt ttc gac gcc gct gca gcc aca gtc tct tct cgt ttg ctt gag cgc 307
Arg Phe Asp Ala Ala Ala Ala Thr Val Ser Ser Arg Leu Leu Glu Arg
55 60 65

tcc gaa gct gct gaa gga cca gca gct gag gtg ctt aaa gct act gct 355
Ser Glu Ala Ala Glu Gly Pro Ala Ala Glu Val Leu Lys Ala Thr Ala
70 75 80 85

ggc atg gtc aat gac cgt ggc tgg cgt aag gct gtc atc aag ggt gtc 403

```
Gly Met Val Asn Asp Arg Gly Trp Arg Lys Ala Val Ile Lys Gly Val
                 90                  95                 100

aag ggt ggt cac cct gcg gaa tac gcc gtg gtt gca gca aca acc aag   451
Lys Gly Gly His Pro Ala Glu Tyr Ala Val Val Ala Ala Thr Thr Lys
            105                 110                 115

ttc atc tcc atg ttc gaa gcc gca ggc ggc ctg atc gcg gag cgc acc   499
Phe Ile Ser Met Phe Glu Ala Ala Gly Gly Leu Ile Ala Glu Arg Thr
        120                 125                 130

aca gac ttg cgc gac atc cgc gac cgc gtc atc gca gaa ctt cgt ggc   547
Thr Asp Leu Arg Asp Ile Arg Asp Arg Val Ile Ala Glu Leu Arg Gly
    135                 140                 145

gat gaa gag cca ggt ctg cca gct gtt tcc gga cag gtc att ctc ttt   595
Asp Glu Glu Pro Gly Leu Pro Ala Val Ser Gly Gln Val Ile Leu Phe
150                 155                 160                 165

gca gat gac ctc tcc cca gca gac acc gcg gca cta gac aca gat ctc   643
Ala Asp Asp Leu Ser Pro Ala Asp Thr Ala Ala Leu Asp Thr Asp Leu
                170                 175                 180

ttt gtg gga ctt gtc act gag ctg ggt ggc cca acg agc cac acc gcg   691
Phe Val Gly Leu Val Thr Glu Leu Gly Gly Pro Thr Ser His Thr Ala
            185                 190                 195

atc atc gca cgc cag ctc aac gtg cct tgc atc gtc gca tcc ggc gcc   739
Ile Ile Ala Arg Gln Leu Asn Val Pro Cys Ile Val Ala Ser Gly Ala
        200                 205                 210

ggc atc aag gac atc aag tcc ggc gaa aag gtg ctt atc gac ggc agc   787
Gly Ile Lys Asp Ile Lys Ser Gly Glu Lys Val Leu Ile Asp Gly Ser
    215                 220                 225

ctc ggc acc att gac cgc aac gcg gac gaa gct gaa gca acc aag ctc   835
Leu Gly Thr Ile Asp Arg Asn Ala Asp Glu Ala Glu Ala Thr Lys Leu
230                 235                 240                 245

gtc tcc gag tcc ctc gag cgc gct gct cgc atc gcc gag tgg aag ggt   883
Val Ser Glu Ser Leu Glu Arg Ala Ala Arg Ile Ala Glu Trp Lys Gly
                250                 255                 260

cct gca caa acc aag gac ggc tac cgc gtt cag ctg ttg gcc aac gtc   931
Pro Ala Gln Thr Lys Asp Gly Tyr Arg Val Gln Leu Leu Ala Asn Val
            265                 270                 275

caa gac ggc aac tct gca cag cag gct gca cag acc gaa gca gaa ggc   979
Gln Asp Gly Asn Ser Ala Gln Gln Ala Ala Gln Thr Glu Ala Glu Gly
        280                 285                 290

atc ggc ctg ttc cgc acc gaa ctg tgc ttc ctt tcc gcc acc gaa gag
1027
Ile Gly Leu Phe Arg Thr Glu Leu Cys Phe Leu Ser Ala Thr Glu Glu
    295                 300                 305

cca agc gtt gat gag cag gct gcg gtc tac tca aag gtg ctt gaa gca
1075
Pro Ser Val Asp Glu Gln Ala Ala Val Tyr Ser Lys Val Leu Glu Ala
310                 315                 320                 325
```

```
ttc cca gag tcc aag gtc gtt gtc cgc tcc ctc gac gca ggt tct gac
1123
Phe Pro Glu Ser Lys Val Val Val Arg Ser Leu Asp Ala Gly Ser Asp
                330                 335                 340

aag cca gtt cca ttc gca tcg atg gct gat gag atg aac cca gca ctg
1171
Lys Pro Val Pro Phe Ala Ser Met Ala Asp Glu Met Asn Pro Ala Leu
            345                 350                 355

ggt gtt cgt ggc ctg cgt atc gca cgt gga cag gtt gat ctg ctg act
1219
Gly Val Arg Gly Leu Arg Ile Ala Arg Gly Gln Val Asp Leu Leu Thr
        360                 365                 370

cgc cag ctc gac gca att gcg aag gcc agc gaa gaa ctc ggc cgt ggc
1267
Arg Gln Leu Asp Ala Ile Ala Lys Ala Ser Glu Glu Leu Gly Arg Gly
    375                 380                 385

gac gac gcc cca acc tgg gtt atg gct cca atg gtg gct acc gct tat
1315
Asp Asp Ala Pro Thr Trp Val Met Ala Pro Met Val Ala Thr Ala Tyr
390                 395                 400                 405

gaa gca aag tgg ttt gct gac atg tgc cgt gag cgt ggc cta atc gcc
1363
Glu Ala Lys Trp Phe Ala Asp Met Cys Arg Glu Arg Gly Leu Ile Ala
                410                 415                 420

ggc gcc atg atc gaa gtt cca gca gca tcc ctg atg gca gac aag atc
1411
Gly Ala Met Ile Glu Val Pro Ala Ala Ser Leu Met Ala Asp Lys Ile
            425                 430                 435

atg cct cac ctg gac ttt gtt tcc atc ggt acc aac gac ctg acc cag
1459
Met Pro His Leu Asp Phe Val Ser Ile Gly Thr Asn Asp Leu Thr Gln
        440                 445                 450

tac acc atg gca gcg gac cgc atg tct cct gag ctt gcc tac ctg acc
1507
Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu Leu Ala Tyr Leu Thr
    455                 460                 465

gat cct tgg cag cca gca gtc ctg cgc ctg atc aag cac acc tgt gac
1555
Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile Lys His Thr Cys Asp
470                 475                 480                 485

gaa ggt gct cgc ttt aac acc ccg gtc ggt gtt tgt ggt gaa gca gca
1603
Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val Cys Gly Glu Ala Ala
                490                 495                 500

gca gac cca ctg ttg gca act gtc ctc acc ggt ctt ggc gtg aac tcc
1651
Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly Leu Gly Val Asn Ser
            505                 510                 515
```

```
ctg tcc gca gca tcc act gct ctc gca gca gtc ggt gca aag ctg tca
1699
Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val Gly Ala Lys Leu Ser
        520                 525                 530

gag gtc acc ctg gaa acc tgt aag aag gca gca gaa gca gca ctt gac
1747
Glu Val Thr Leu Glu Thr Cys Lys Lys Ala Ala Glu Ala Ala Leu Asp
    535                 540                 545

gct gaa ggt gca act gaa gca cgc gat gct gta cgc gca gtg atc gac
1795
Ala Glu Gly Ala Thr Glu Ala Arg Asp Ala Val Arg Ala Val Ile Asp
550                 555                 560                 565

gca gca gtc taaaccactg ttgagctaaa aag
1827
Ala Ala Val
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<210> 18
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 18

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Val Ala Thr Val Ala Asp Val Asn Gln Asp Thr Val Leu Lys Gly Thr
  1               5                  10                  15

Gly Val Val Gly Gly Val Arg Tyr Ala Ser Ala Val Trp Ile Thr Pro
             20                  25                  30

Arg Pro Glu Leu Pro Gln Ala Gly Glu Val Val Ala Glu Glu Asn Arg
         35                  40                  45

Glu Ala Glu Gln Glu Arg Phe Asp Ala Ala Ala Ala Thr Val Ser Ser
     50                  55                  60

Arg Leu Leu Glu Arg Ser Glu Ala Ala Glu Gly Pro Ala Ala Glu Val
 65                  70                  75                  80

Leu Lys Ala Thr Ala Gly Met Val Asn Asp Arg Gly Trp Arg Lys Ala
                 85                  90                  95

Val Ile Lys Gly Val Lys Gly Gly His Pro Ala Glu Tyr Ala Val Val
            100                 105                 110

Ala Ala Thr Thr Lys Phe Ile Ser Met Phe Glu Ala Ala Gly Gly Leu
        115                 120                 125

Ile Ala Glu Arg Thr Thr Asp Leu Arg Asp Ile Arg Asp Arg Val Ile
    130                 135                 140

Ala Glu Leu Arg Gly Asp Glu Glu Pro Gly Leu Pro Ala Val Ser Gly
145                 150                 155                 160

Gln Val Ile Leu Phe Ala Asp Asp Leu Ser Pro Ala Asp Thr Ala Ala
                165                 170                 175

Leu Asp Thr Asp Leu Phe Val Gly Leu Val Thr Glu Leu Gly Gly Pro
```

```
            180                 185                 190

Thr Ser His Thr Ala Ile Ile Ala Arg Gln Leu Asn Val Pro Cys Ile
        195                 200                 205

Val Ala Ser Gly Ala Gly Ile Lys Asp Ile Lys Ser Gly Glu Lys Val
    210                 215                 220

Leu Ile Asp Gly Ser Leu Gly Thr Ile Asp Arg Asn Ala Asp Glu Ala
225                 230                 235                 240

Glu Ala Thr Lys Leu Val Ser Glu Ser Leu Glu Arg Ala Ala Arg Ile
                245                 250                 255

Ala Glu Trp Lys Gly Pro Ala Gln Thr Lys Asp Gly Tyr Arg Val Gln
            260                 265                 270

Leu Leu Ala Asn Val Gln Asp Gly Asn Ser Ala Gln Gln Ala Ala Gln
        275                 280                 285

Thr Glu Ala Glu Gly Ile Gly Leu Phe Arg Thr Glu Leu Cys Phe Leu
    290                 295                 300

Ser Ala Thr Glu Glu Pro Ser Val Asp Glu Gln Ala Ala Val Tyr Ser
305                 310                 315                 320

Lys Val Leu Glu Ala Phe Pro Glu Ser Lys Val Val Val Arg Ser Leu
                325                 330                 335

Asp Ala Gly Ser Asp Lys Pro Val Pro Phe Ala Ser Met Ala Asp Glu
            340                 345                 350

Met Asn Pro Ala Leu Gly Val Arg Gly Leu Arg Ile Ala Arg Gly Gln
        355                 360                 365

Val Asp Leu Leu Thr Arg Gln Leu Asp Ala Ile Ala Lys Ala Ser Glu
    370                 375                 380

Glu Leu Gly Arg Gly Asp Asp Ala Pro Thr Trp Val Met Ala Pro Met
385                 390                 395                 400

Val Ala Thr Ala Tyr Glu Ala Lys Trp Phe Ala Asp Met Cys Arg Glu
                405                 410                 415

Arg Gly Leu Ile Ala Gly Ala Met Ile Glu Val Pro Ala Ala Ser Leu
            420                 425                 430

Met Ala Asp Lys Ile Met Pro His Leu Asp Phe Val Ser Ile Gly Thr
        435                 440                 445

Asn Asp Leu Thr Gln Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu
    450                 455                 460

Leu Ala Tyr Leu Thr Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile
465                 470                 475                 480

Lys His Thr Cys Asp Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val
                485                 490                 495

Cys Gly Glu Ala Ala Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly
            500                 505                 510
```

Leu Gly Val Asn Ser Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val
515 520 525

Gly Ala Lys Leu Ser Glu Val Thr Leu Glu Thr Cys Lys Lys Ala Ala
530 535 540

Glu Ala Ala Leu Asp Ala Glu Gly Ala Thr Glu Ala Arg Asp Ala Val
545 550 555 560

Arg Ala Val Ile Asp Ala Ala Val
565

<210> 19
<211> 1629
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (98)..(1606)
<223> FRXA01244

<400> 19
agatgtcgat ttctcgagga agaagttaac gccgaagaaa accgtgaatc agagcaggag 60

cgcttcgacg ccgctgcagc cacagtctct tcttcgtttg ctt gag cgc tcc gaa 115
Leu Leu Glu Arg Ser Glu
1 5

gct gct gaa gga cca gca gct gag gtg ctt aaa gct act gct ggc atg 163
Ala Ala Glu Gly Pro Ala Ala Glu Val Leu Lys Ala Thr Ala Gly Met
10 15 20

gtc aat gac cgt ggc tgg cgt aag gct gtc atc aag ggt gtc aag ggt 211
Val Asn Asp Arg Gly Trp Arg Lys Ala Val Ile Lys Gly Val Lys Gly
25 30 35

ggt cac cct gcg gaa tac gcc gtg gtt gca gca aca acc aag ttc atc 259
Gly His Pro Ala Glu Tyr Ala Val Val Ala Ala Thr Thr Lys Phe Ile
40 45 50

tcc atg ttc gaa gcc gca ggc ggc ctg atc gcg gag cgc acc aca gac 307
Ser Met Phe Glu Ala Ala Gly Gly Leu Ile Ala Glu Arg Thr Thr Asp
55 60 65 70

ttg cgc gac atc cgc gac cgc gtc atc gca gaa ctt cgt ggc gat gaa 355
Leu Arg Asp Ile Arg Asp Arg Val Ile Ala Glu Leu Arg Gly Asp Glu
75 80 85

gag cca ggt ctg cca gct gtt tcc gga cag gtc att ctc ttt gca gat 403
Glu Pro Gly Leu Pro Ala Val Ser Gly Gln Val Ile Leu Phe Ala Asp
90 95 100

gac ctc tcc cca gca gac acc gcg gca cta gac aca gat ctc ttt gtg 451
Asp Leu Ser Pro Ala Asp Thr Ala Ala Leu Asp Thr Asp Leu Phe Val
105 110 115

gga ctt gtc act gag ctg ggt ggc cca acg agc cac acc gcg atc atc 499
Gly Leu Val Thr Glu Leu Gly Gly Pro Thr Ser His Thr Ala Ile Ile

```
    120                 125                 130

gca cgc cag ctc aac gtg cct tgc atc gtc gca tcc ggc gcc ggc atc   547
Ala Arg Gln Leu Asn Val Pro Cys Ile Val Ala Ser Gly Ala Gly Ile
135                 140                 145                 150

aag gac atc aag tcc ggc gaa aag gtg ctt atc gac ggc agc ctc ggc   595
Lys Asp Ile Lys Ser Gly Glu Lys Val Leu Ile Asp Gly Ser Leu Gly
                155                 160                 165

acc att gac cgc aac gcg gac gaa gct gaa gca acc aag ctc gtc tcc   643
Thr Ile Asp Arg Asn Ala Asp Glu Ala Glu Ala Thr Lys Leu Val Ser
            170                 175                 180

gag tcc ctc gag cgc gct gct cgc atc gcc gag tgg aag ggt cct gca   691
Glu Ser Leu Glu Arg Ala Ala Arg Ile Ala Glu Trp Lys Gly Pro Ala
        185                 190                 195

caa acc aag gac ggc tac cgc gtt cag ctg ttg gcc aac gtc caa gac   739
Gln Thr Lys Asp Gly Tyr Arg Val Gln Leu Leu Ala Asn Val Gln Asp
    200                 205                 210

ggc aac tct gca cag cag gct gca cag acc gaa gca gaa ggc atc ggc   787
Gly Asn Ser Ala Gln Gln Ala Ala Gln Thr Glu Ala Glu Gly Ile Gly
215                 220                 225                 230

ctg ttc cgc acc gaa ctg tgc ttc ctt tcc gcc acc gaa gag cca agc   835
Leu Phe Arg Thr Glu Leu Cys Phe Leu Ser Ala Thr Glu Glu Pro Ser
                235                 240                 245

gtt gat gag cag gct gcg gtc tac tca aag gtg ctt gaa gca ttc cca   883
Val Asp Glu Gln Ala Ala Val Tyr Ser Lys Val Leu Glu Ala Phe Pro
            250                 255                 260

gag tcc aag gtc gtt gtc cgc tcc ctc gac gca ggt tct gac aag cca   931
Glu Ser Lys Val Val Val Arg Ser Leu Asp Ala Gly Ser Asp Lys Pro
        265                 270                 275

gtt cca ttc gca tcg atg gct gat gag atg aac cca gca ctg ggt gtt   979
Val Pro Phe Ala Ser Met Ala Asp Glu Met Asn Pro Ala Leu Gly Val
    280                 285                 290

cgt ggc ctg cgt atc gca cgt gga cag gtt gat ctg ctg act cgc cag
1027
Arg Gly Leu Arg Ile Ala Arg Gly Gln Val Asp Leu Leu Thr Arg Gln
295                 300                 305                 310

ctc gac gca att gcg aag gcc agc gaa gaa ctc ggc cgt ggc gac gac
1075
Leu Asp Ala Ile Ala Lys Ala Ser Glu Glu Leu Gly Arg Gly Asp Asp
                315                 320                 325

gcc cca acc tgg gtt atg gct cca atg gtg gct acc gct tat gaa gca
1123
Ala Pro Thr Trp Val Met Ala Pro Met Val Ala Thr Ala Tyr Glu Ala
            330                 335                 340

aag tgg ttt gct gac atg tgc cgt gag cgt ggc cta atc gcc ggc gcc
1171
Lys Trp Phe Ala Asp Met Cys Arg Glu Arg Gly Leu Ile Ala Gly Ala
        345                 350                 355
```

atg atc gaa gtt cca gca gca tcc ctg atg gca gac aag atc atg cct
1219
Met Ile Glu Val Pro Ala Ala Ser Leu Met Ala Asp Lys Ile Met Pro
360 365 370

cac ctg gac ttt gtt tcc atc ggt acc aac gac ctg acc cag tac acc
1267
His Leu Asp Phe Val Ser Ile Gly Thr Asn Asp Leu Thr Gln Tyr Thr
375 380 385 390

atg gca gcg gac cgc atg tct cct gag ctt gcc tac ctg acc gat cct
1315
Met Ala Ala Asp Arg Met Ser Pro Glu Leu Ala Tyr Leu Thr Asp Pro
395 400 405

tgg cag cca gca gtc ctg cgc ctg atc aag cac acc tgt gac gaa ggt
1363
Trp Gln Pro Ala Val Leu Arg Leu Ile Lys His Thr Cys Asp Glu Gly
410 415 420

gct cgc ttt aac acc ccg gtc ggt gtt tgt ggt gaa gca gca gca gac
1411
Ala Arg Phe Asn Thr Pro Val Gly Val Cys Gly Glu Ala Ala Ala Asp
425 430 435

cca ctg ttg gca act gtc ctc acc ggt ctt ggc gtg aac tcc ctg tcc
1459
Pro Leu Leu Ala Thr Val Leu Thr Gly Leu Gly Val Asn Ser Leu Ser
440 445 450

gca gca tcc act gct ctc gca gca gtc ggt gca aag ctg tca gag gtc
1507
Ala Ala Ser Thr Ala Leu Ala Ala Val Gly Ala Lys Leu Ser Glu Val
455 460 465 470

acc ctg gaa acc tgt aag aag gca gca gaa gca gca ctt gac gct gaa
1555
Thr Leu Glu Thr Cys Lys Lys Ala Ala Glu Ala Ala Leu Asp Ala Glu
475 480 485

ggt gca act gaa gca cgc gat gct gta cgc gca gtg atc gac gca gca
1603
Gly Ala Thr Glu Ala Arg Asp Ala Val Arg Ala Val Ile Asp Ala Ala
490 495 500

gtc taaaccactg ttgagctaaa aag
1629
Val

<210> 20
<211> 503
<212> PRT
<213> Corynebacterium glutamicum

<400> 20
Leu Leu Glu Arg Ser Glu Ala Ala Glu Gly Pro Ala Ala Glu Val Leu
1 5 10 15

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Lys Ala Thr Ala Gly Met Val Asn Asp Arg Gly Trp Arg Lys Ala Val
             20                  25                  30

Ile Lys Gly Val Lys Gly Gly His Pro Ala Glu Tyr Ala Val Val Ala
         35                  40                  45

Ala Thr Thr Lys Phe Ile Ser Met Phe Glu Ala Ala Gly Gly Leu Ile
     50                  55                  60

Ala Glu Arg Thr Thr Asp Leu Arg Asp Ile Arg Asp Arg Val Ile Ala
 65                  70                  75                  80

Glu Leu Arg Gly Asp Glu Glu Pro Gly Leu Pro Ala Val Ser Gly Gln
                 85                  90                  95

Val Ile Leu Phe Ala Asp Asp Leu Ser Pro Ala Asp Thr Ala Ala Leu
            100                 105                 110

Asp Thr Asp Leu Phe Val Gly Leu Val Thr Glu Leu Gly Gly Pro Thr
        115                 120                 125

Ser His Thr Ala Ile Ile Ala Arg Gln Leu Asn Val Pro Cys Ile Val
    130                 135                 140

Ala Ser Gly Ala Gly Ile Lys Asp Ile Lys Ser Gly Glu Lys Val Leu
145                 150                 155                 160

Ile Asp Gly Ser Leu Gly Thr Ile Asp Arg Asn Ala Asp Glu Ala Glu
                165                 170                 175

Ala Thr Lys Leu Val Ser Glu Ser Leu Glu Arg Ala Ala Arg Ile Ala
            180                 185                 190

Glu Trp Lys Gly Pro Ala Gln Thr Lys Asp Gly Tyr Arg Val Gln Leu
        195                 200                 205

Leu Ala Asn Val Gln Asp Gly Asn Ser Ala Gln Gln Ala Ala Gln Thr
    210                 215                 220

Glu Ala Glu Gly Ile Gly Leu Phe Arg Thr Glu Leu Cys Phe Leu Ser
225                 230                 235                 240

Ala Thr Glu Glu Pro Ser Val Asp Glu Gln Ala Ala Val Tyr Ser Lys
                245                 250                 255

Val Leu Glu Ala Phe Pro Glu Ser Lys Val Val Val Arg Ser Leu Asp
            260                 265                 270

Ala Gly Ser Asp Lys Pro Val Pro Phe Ala Ser Met Ala Asp Glu Met
        275                 280                 285

Asn Pro Ala Leu Gly Val Arg Gly Leu Arg Ile Ala Arg Gly Gln Val
    290                 295                 300

Asp Leu Leu Thr Arg Gln Leu Asp Ala Ile Ala Lys Ala Ser Glu Glu
305                 310                 315                 320

Leu Gly Arg Gly Asp Asp Ala Pro Thr Trp Val Met Ala Pro Met Val
                325                 330                 335

Ala Thr Ala Tyr Glu Ala Lys Trp Phe Ala Asp Met Cys Arg Glu Arg
```

```
            340                 345                 350

Gly Leu Ile Ala Gly Ala Met Ile Glu Val Pro Ala Ala Ser Leu Met
        355                 360                 365

Ala Asp Lys Ile Met Pro His Leu Asp Phe Val Ser Ile Gly Thr Asn
    370                 375                 380

Asp Leu Thr Gln Tyr Thr Met Ala Ala Asp Arg Met Ser Pro Glu Leu
385                 390                 395                 400

Ala Tyr Leu Thr Asp Pro Trp Gln Pro Ala Val Leu Arg Leu Ile Lys
                405                 410                 415

His Thr Cys Asp Glu Gly Ala Arg Phe Asn Thr Pro Val Gly Val Cys
            420                 425                 430

Gly Glu Ala Ala Ala Asp Pro Leu Leu Ala Thr Val Leu Thr Gly Leu
        435                 440                 445

Gly Val Asn Ser Leu Ser Ala Ala Ser Thr Ala Leu Ala Ala Val Gly
    450                 455                 460

Ala Lys Leu Ser Glu Val Thr Leu Glu Thr Cys Lys Lys Ala Ala Glu
465                 470                 475                 480

Ala Ala Leu Asp Ala Glu Gly Ala Thr Glu Ala Arg Asp Ala Val Arg
                485                 490                 495

Ala Val Ile Asp Ala Ala Val
            500
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<210> 21
<211> 390
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(367)
<223> RXA01300

<400> 21
gatcgacatt aaatcccctc ccttgggggg tttaactaac aaatcgctgc gccctaatcc 60

gttcggatta acggcgtagc aacacgaaag gacactttcc atg gct tcc aag act   115
                                            Met Ala Ser Lys Thr
                                              1               5

gta acc gtc ggt tcc tcc gtt ggc ctg cac gca cgt cca gca tcc atc   163
Val Thr Val Gly Ser Ser Val Gly Leu His Ala Arg Pro Ala Ser Ile
                 10                  15                  20

atc gct gaa gcg gct gct gag tac gac gac gaa atc ttg ctg acc ctg   211
Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu Ile Leu Leu Thr Leu
             25                  30                  35

gtt ggc tcc gat gat gac gaa gag acc gac gcg tcc tct tcc ctc atg   259
Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala Ser Ser Ser Leu Met
         40                  45                  50
```

```
atc atg gcg ctg ggc gca gag cac ggc aac gaa gtt acc gtc acc tcc   307
Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu Val Thr Val Thr Ser
     55                  60                  65

gac aac gct gaa gct gtt gag aag atc gct gcg ctt atc gca cag gac   355
Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala Leu Ile Ala Gln Asp
 70                  75                  80                  85

ctt gac gct gag taaacaacgc tctgcttgtt aaa                        390
Leu Asp Ala Glu
```

<210> 22
<211> 89
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Met Ala Ser Lys Thr Val Thr Val Gly Ser Ser Val Gly Leu His Ala
  1               5                  10                  15

Arg Pro Ala Ser Ile Ile Ala Glu Ala Ala Ala Glu Tyr Asp Asp Glu
             20                  25                  30

Ile Leu Leu Thr Leu Val Gly Ser Asp Asp Asp Glu Glu Thr Asp Ala
         35                  40                  45

Ser Ser Ser Leu Met Ile Met Ala Leu Gly Ala Glu His Gly Asn Glu
     50                  55                  60

Val Thr Val Thr Ser Asp Asn Ala Glu Ala Val Glu Lys Ile Ala Ala
 65                  70                  75                  80

Leu Ile Ala Gln Asp Leu Asp Ala Glu
                 85
```

<210> 23
<211> 508
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(508)
<223> RXN03002

<400> 23

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ggaacttcga ggtgtcttcg tggggcgtac ggagatctag caagtgtggc tttatgtttg 60

accctatccg aatcaacatg cagtgaatta acatctactt atg ttt gta ctc aaa   115
                                               Met Phe Val Leu Lys
                                                 1               5

gat ctg cta aag gca gaa cgc ata gaa ctc gac cgc acg gtc acc gat   163
Asp Leu Leu Lys Ala Glu Arg Ile Glu Leu Asp Arg Thr Val Thr Asp
                 10                  15                  20

tgg cgt gaa ggc atc cgc gcc gca ggt gta ctc cta gaa aag aca aac   211
```

```
Trp Arg Glu Gly Ile Arg Ala Ala Gly Val Leu Leu Glu Lys Thr Asn
             25                  30                  35

agc att gat tcc gcc tac acc gat gcc atg atc gcc agc gtg gaa gaa   259
Ser Ile Asp Ser Ala Tyr Thr Asp Ala Met Ile Ala Ser Val Glu Glu
         40                  45                  50

aaa ggc ccc tac att gtg gtc gct cca ggt ttc gct ttc gcg cac gcc   307
Lys Gly Pro Tyr Ile Val Val Ala Pro Gly Phe Ala Phe Ala His Ala
     55                  60                  65

cgc ccc agc aga gca gtc cgc gag acc gct atg tcg tgg gtg cgc ctg   355
Arg Pro Ser Arg Ala Val Arg Glu Thr Ala Met Ser Trp Val Arg Leu
 70                  75                  80                  85

gcc tcc cct gtt tcc ttc ggt cac agt aag aat gat ccc ctc aat ctc   403
Ala Ser Pro Val Ser Phe Gly His Ser Lys Asn Asp Pro Leu Asn Leu
                 90                  95                 100

atc gtt gct ctc gct gcc aaa gat gcc acc gca cat acc caa gcg atg   451
Ile Val Ala Leu Ala Ala Lys Asp Ala Thr Ala His Thr Gln Ala Met
            105                 110                 115

gcg gca ttg gct aaa gct tta gga aaa tac cga aag gat ctc gac gag   499
Ala Ala Leu Ala Lys Ala Leu Gly Lys Tyr Arg Lys Asp Leu Asp Glu
        120                 125                 130

gca caa agt                                                      508
Ala Gln Ser
    135
```

<210> 24
<211> 136
<212> PRT
<213> Corynebacterium glutamicum

<400> 24

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Met Phe Val Leu Lys Asp Leu Leu Lys Ala Glu Arg Ile Glu Leu Asp
  1               5                  10                  15

Arg Thr Val Thr Asp Trp Arg Glu Gly Ile Arg Ala Ala Gly Val Leu
             20                  25                  30

Leu Glu Lys Thr Asn Ser Ile Asp Ser Ala Tyr Thr Asp Ala Met Ile
         35                  40                  45

Ala Ser Val Glu Glu Lys Gly Pro Tyr Ile Val Val Ala Pro Gly Phe
     50                  55                  60

Ala Phe Ala His Ala Arg Pro Ser Arg Ala Val Arg Glu Thr Ala Met
 65                  70                  75                  80

Ser Trp Val Arg Leu Ala Ser Pro Val Ser Phe Gly His Ser Lys Asn
                 85                  90                  95

Asp Pro Leu Asn Leu Ile Val Ala Leu Ala Ala Lys Asp Ala Thr Ala
            100                 105                 110

His Thr Gln Ala Met Ala Ala Leu Ala Lys Ala Leu Gly Lys Tyr Arg
        115                 120                 125
```

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Lys Asp Leu Asp Glu Ala Gln Ser
    130                 135


<210> 25
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (14)..(766)
<223> RXC00953

<400> 25
cttgcattcc ccaatg gcg cca cca acg gta ggc aac tac atc atg cag tcc 52
              Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser
                1               5                  10

ttc act caa ggt ctg cag ttc ggc gtt gca gtt gcc gtg att ctc ttt   100
Phe Thr Gln Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe
     15                  20                  25

ggt gtc cgc acc att ctt ggt gaa ctg gtc ccc gca ttc caa ggt att   148
Gly Val Arg Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile
 30                  35                  40                  45

gct gcg aag gtt gtt ccc gga gct atc ccc gca ttg gat gca ccg atc   196
Ala Ala Lys Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile
                 50                  55                  60

gtg ttc ccc tac gcg cag aac gcc gtt ctc att ggt ttc ttg tct tcc   244
Val Phe Pro Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser
             65                  70                  75

ttc gtc ggt ggc ttg gtt ggc ctg act gtt ctt gca tcg tgg ctg aac   292
Phe Val Gly Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn
         80                  85                  90

cca gct ttt ggt gtc gcg ttg att ctg cct ggt ttg gtc ccc cac ttc   340
Pro Ala Phe Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe
     95                  100                 105

ttc act ggt ggc gcg gcg ggc gtt tac ggt aat gcc acg ggt ggt cgt   388
Phe Thr Gly Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg
110                 115                 120                 125

cga gga gca gta ttt ggc gcc ttt gcc aac ggt ctt ctg att acc ttc   436
Arg Gly Ala Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe
                130                 135                 140

ctc cct gct ttc ctg ctt ggt gtg ctt ggt tcc ttc ggg tca gag aac   484
Leu Pro Ala Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn
            145                 150                 155

acc act ttc ggt gat gcg gac ttt ggt tgg ttc gga atc gtt gtt ggt   532
Thr Thr Phe Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly
        160                 165                 170

tct gca gcc aag gtg gaa ggt gct ggc ggg ctc atc ttg ttg ctc atc   580
```

```
Ser Ala Ala Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile
    175                 180                 185

atc gca gcg gtt ctt ctg ggt ggc gcg atg gtc ttc cag aag cgc gtc   628
Ile Ala Ala Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val
190                 195                 200                 205

gtg aat ggg cac tgg gat cca gct ccc aac cgt gag cgc gtg gag aag   676
Val Asn Gly His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys
                210                 215                 220

gcg gaa gct gat gcc act cca acg gct ggg gct cgg acc tac cct aag   724
Ala Glu Ala Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys
            225                 230                 235

att gct cct ccg gcg ggc gct cct acc cca ccg gct cga agc           766
Ile Ala Pro Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
        240                 245                 250

taagatctcc aaaaccctga gat                                        789
```

<210> 26
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 26

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Met Ala Pro Pro Thr Val Gly Asn Tyr Ile Met Gln Ser Phe Thr Gln
  1               5                  10                  15

Gly Leu Gln Phe Gly Val Ala Val Ala Val Ile Leu Phe Gly Val Arg
             20                  25                  30

Thr Ile Leu Gly Glu Leu Val Pro Ala Phe Gln Gly Ile Ala Ala Lys
         35                  40                  45

Val Val Pro Gly Ala Ile Pro Ala Leu Asp Ala Pro Ile Val Phe Pro
     50                  55                  60

Tyr Ala Gln Asn Ala Val Leu Ile Gly Phe Leu Ser Ser Phe Val Gly
 65                  70                  75                  80

Gly Leu Val Gly Leu Thr Val Leu Ala Ser Trp Leu Asn Pro Ala Phe
                 85                  90                  95

Gly Val Ala Leu Ile Leu Pro Gly Leu Val Pro His Phe Phe Thr Gly
            100                 105                 110

Gly Ala Ala Gly Val Tyr Gly Asn Ala Thr Gly Gly Arg Arg Gly Ala
        115                 120                 125

Val Phe Gly Ala Phe Ala Asn Gly Leu Leu Ile Thr Phe Leu Pro Ala
    130                 135                 140

Phe Leu Leu Gly Val Leu Gly Ser Phe Gly Ser Glu Asn Thr Thr Phe
145                 150                 155                 160

Gly Asp Ala Asp Phe Gly Trp Phe Gly Ile Val Val Gly Ser Ala Ala
                165                 170                 175
```

```
Lys Val Glu Gly Ala Gly Gly Leu Ile Leu Leu Leu Ile Ile Ala Ala
            180                 185                 190

Val Leu Leu Gly Gly Ala Met Val Phe Gln Lys Arg Val Val Asn Gly
        195                 200                 205

His Trp Asp Pro Ala Pro Asn Arg Glu Arg Val Glu Lys Ala Glu Ala
    210                 215                 220

Asp Ala Thr Pro Thr Ala Gly Ala Arg Thr Tyr Pro Lys Ile Ala Pro
225                 230                 235                 240

Pro Ala Gly Ala Pro Thr Pro Pro Ala Arg Ser
                245                 250


<210> 27
<211> 553
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(553)
<223> RXC03001

<400> 27
cccggttcac gtgatcaatg acttcacgag caccgatgaa atcgatgctg cgcttcgtga 60

acgctacgac atctaactac tttaaaagga cgaaaatatt atg gac tgg tta acc   115
                                            Met Asp Trp Leu Thr
                                              1               5

att cct ctt ttc ctc gtt aat gaa atc ctt gcg gtt ccg gct ttc ctc   163
Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala Val Pro Ala Phe Leu
                10                  15                  20

atc ggt atc atc acc gcc gtg gga ttg ggt gcc atg ggg cgt tcc gtc   211
Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala Met Gly Arg Ser Val
            25                  30                  35

ggt cag gtt atc ggt gga gca atc aaa gca acg ttg ggc ttt ttg ctc   259
Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr Leu Gly Phe Leu Leu
        40                  45                  50

att ggt gcg ggt gcc acg ttg gtc act gcc tcc ctg gag cca ctg ggt   307
Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser Leu Glu Pro Leu Gly
    55                  60                  65

gcg atg atc atg ggt gcc aca ggc atg cgt ggt gtt gtc cca acg aat   355
Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly Val Val Pro Thr Asn
70                  75                  80                  85

gaa gcc atc gcc gga atc gca cag gct gaa tac ggc gcg cag gtg gcg   403
Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr Gly Ala Gln Val Ala
                90                  95                  100

tgg ctg atg att ctg ggc ttc gcc atc tct ttg gtg ttg gct cgt ttc   451
Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu Val Leu Ala Arg Phe
            105                 110                 115
```

```
acc aac ctg cgt tat gtc ttg ctc aac gga cac cac gtg ctg ttg atg   499
Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His His Val Leu Leu Met
        120                 125                 130

tgc acc atg ctc acc atg gtc ttg gcc acc gga aga gtt gat gcg tgg   547
Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly Arg Val Asp Ala Trp
    135                 140                 145

atc ttc                                                           553
Ile Phe
150
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<210> 28
<211> 151
<212> PRT
<213> Corynebacterium glutamicum

<400> 28

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Met Asp Trp Leu Thr Ile Pro Leu Phe Leu Val Asn Glu Ile Leu Ala
  1               5                  10                  15

Val Pro Ala Phe Leu Ile Gly Ile Ile Thr Ala Val Gly Leu Gly Ala
             20                  25                  30

Met Gly Arg Ser Val Gly Gln Val Ile Gly Gly Ala Ile Lys Ala Thr
         35                  40                  45

Leu Gly Phe Leu Leu Ile Gly Ala Gly Ala Thr Leu Val Thr Ala Ser
     50                  55                  60

Leu Glu Pro Leu Gly Ala Met Ile Met Gly Ala Thr Gly Met Arg Gly
 65                  70                  75                  80

Val Val Pro Thr Asn Glu Ala Ile Ala Gly Ile Ala Gln Ala Glu Tyr
                85                  90                  95

Gly Ala Gln Val Ala Trp Leu Met Ile Leu Gly Phe Ala Ile Ser Leu
            100                 105                 110

Val Leu Ala Arg Phe Thr Asn Leu Arg Tyr Val Leu Leu Asn Gly His
        115                 120                 125

His Val Leu Leu Met Cys Thr Met Leu Thr Met Val Leu Ala Thr Gly
    130                 135                 140

Arg Val Asp Ala Trp Ile Phe
145                 150
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<210> 29
<211> 2172
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2149)
<223> RXN01943

<400> 29

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ccgattcttt ttcggcccaa ttcgtaacgg cgatcctctt aagtggacaa gaaagtctct 60

tgcccgcggg agacagaccc tacgtttaga aaggtttgac atg gcg tcc aaa ctg   115
                                            Met Ala Ser Lys Leu
                                              1               5

acg acg aca tcg caa cat att ctg gaa aac ctt ggt gga cca gac aat   163
Thr Thr Thr Ser Gln His Ile Leu Glu Asn Leu Gly Gly Pro Asp Asn
                  10                  15                  20

att act tcg atg act cac tgt gcg act cgc ctt cgc ttc caa gtg aag   211
Ile Thr Ser Met Thr His Cys Ala Thr Arg Leu Arg Phe Gln Val Lys
              25                  30                  35

gat caa tcc att gtt gat caa caa gaa att gac tcc gac cca tca gtt   259
Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp Ser Asp Pro Ser Val
          40                  45                  50

ctt ggc gta gta ccc caa gga tcc acc ggt atg cag gtg gtg atg ggt   307
Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met Gln Val Val Met Gly
      55                  60                  65

gga tct gtt gca aac tat tac caa gaa atc ctc aaa ctt gat gga atg   355
Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu Lys Leu Asp Gly Met
  70                  75                  80                  85

aag cac ttc gcc gac ggt gaa gct aca gag agt tca tcc aag aag gaa   403
Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser Ser Ser Lys Lys Glu
                  90                  95                 100

tac ggc gga gtc cgt ggc aag tac tcg tgg att gac tac gcc ttc gag   451
Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile Asp Tyr Ala Phe Glu
              105                 110                 115

ttc ttg tct gat act ttc cga cca atc ctg tgg gcc ctg ctt ggt gcc   499
Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp Ala Leu Leu Gly Ala
          120                 125                 130

tca ctg att att acc ttg ttg gtt ctt gcg gat act ttc ggt ttg caa   547
Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp Thr Phe Gly Leu Gln
      135                 140                 145

gac ttc cgc gct cca atg gat gag cag cct gat act tat gta ttc ctg   595
Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp Thr Tyr Val Phe Leu
  150                 155                 160                 165

cac tcc atg tgg cgc tcg gtc ttc tac ttc ctg cca att atg gtt ggt   643
His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu Pro Ile Met Val Gly
                  170                 175                 180

gcc acc gca gct cga aag ctc ggc gca aac gag tgg att ggt gca gct   691
Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu Trp Ile Gly Ala Ala
              185                 190                 195

att cca gcc gca ctt ctt act cca gaa ttc ttg gca ctg ggt tct gcc   739
Ile Pro Ala Ala Leu Leu Thr Pro Glu Phe Leu Ala Leu Gly Ser Ala
          200                 205                 210

ggc gat acc gtc aca gtc ttt ggc ctg cca atg gtt ctg aat gac tac   787
Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met Val Leu Asn Asp Tyr
      215                 220                 225
```

```
tcc gga cag gta ttc cca ccg ctg att gca gca att ggt ctg tac tgg   835
Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala Ile Gly Leu Tyr Trp
230                 235                 240                 245

gtg gaa aag gga ctg aag aag atc atc cct gaa gca gtc caa atg gtg   883
Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu Ala Val Gln Met Val
                250                 255                 260

ttc gtc cca ttc ttc tcc ctg ctg att atg atc cca gcg acc gca ttc   931
Phe Val Pro Phe Phe Ser Leu Leu Ile Met Ile Pro Ala Thr Ala Phe
            265                 270                 275

ctg ctt gga cct ttc ggc atc ggt gtt ggt aac gga att tcc aac ctg   979
Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn Gly Ile Ser Asn Leu
        280                 285                 290

ctt gaa gcg att aac aac ttc agc cca ttt att ctt tcc atc gtt atc
1027
Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile Leu Ser Ile Val Ile
    295                 300                 305

cca ttg ctc tac cca ttc ttg gtt cca ctt gga ttg cac tgg cca cta
1075
Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly Leu His Trp Pro Leu
310                 315                 320                 325

aac gcc atc atg atc cag aac atc aac acc ctg ggt tac gac ttc att
1123
Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu Gly Tyr Asp Phe Ile
                330                 335                 340

cag gga cca atg ggt gcc tgg aac ttc gcc tgc ttc ggc ctg gtc acc
1171
Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys Phe Gly Leu Val Thr
            345                 350                 355

ggc gtg ttc ttg ctc tcc att aag gaa cga aac aag gcc atg cgt cag
1219
Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn Lys Ala Met Arg Gln
        360                 365                 370

gtt tcc ctg ggt ggc atg ttg gct ggt ttg ctc ggc ggc att tcc gag
1267
Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu Gly Gly Ile Ser Glu
    375                 380                 385

cct tcc ctc tac ggt gtt ctg ctc cga ttc aag aag acc tac ttc cgc
1315
Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys Lys Thr Tyr Phe Arg
390                 395                 400                 405

ctc ctg ccg ggt tgt ttg gca ggc ggt atc gtg atg ggc atc ttc gac
1363
Leu Leu Pro Gly Cys Leu Ala Gly Gly Ile Val Met Gly Ile Phe Asp
                410                 415                 420

atc aag gcg tac gct ttc gtg ttc acc tcc ttg ctt acc atc cca gca
1411
Ile Lys Ala Tyr Ala Phe Val Phe Thr Ser Leu Leu Thr Ile Pro Ala
            425                 430                 435
```

```
atg gac cca tgg ttg ggc tac acc att ggt atc gca gtt gca ttc ttc
1459
Met Asp Pro Trp Leu Gly Tyr Thr Ile Gly Ile Ala Val Ala Phe Phe
        440                 445                 450

gtt tcc atg ttc ctt gtt ctc gca ctg gac tac cgt tcc aac gaa gag
1507
Val Ser Met Phe Leu Val Leu Ala Leu Asp Tyr Arg Ser Asn Glu Glu
    455                 460                 465

cgc gat gag gca cgt gca aag gtt gct gct gac aag cag gca gaa gaa
1555
Arg Asp Glu Ala Arg Ala Lys Val Ala Ala Asp Lys Gln Ala Glu Glu
470                 475                 480                 485

gat ctg aag gca gaa gct aat gca act cct gca gct cca gta gct gct
1603
Asp Leu Lys Ala Glu Ala Asn Ala Thr Pro Ala Ala Pro Val Ala Ala
                490                 495                 500

gca ggt gcg gga gcc ggt gca ggt gca gga gcc gct gct ggc gct gca
1651
Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Ala Ala Gly Ala Ala
            505                 510                 515

acc gcc gtg gca gct aag ccg aag ctg gcc gct ggg gaa gta gtg gac
1699
Thr Ala Val Ala Ala Lys Pro Lys Leu Ala Ala Gly Glu Val Val Asp
        520                 525                 530

att gtt tcc cca ctc gaa ggc aag gca att cca ctt tct gaa gta cct
1747
Ile Val Ser Pro Leu Glu Gly Lys Ala Ile Pro Leu Ser Glu Val Pro
    535                 540                 545

gac cca atc ttt gca gca ggc aag ctt gga cca ggc att gca atc caa
1795
Asp Pro Ile Phe Ala Ala Gly Lys Leu Gly Pro Gly Ile Ala Ile Gln
550                 555                 560                 565

cca act gga aac acc gtt gtt gct cca gca gac gct act gtc atc ctt
1843
Pro Thr Gly Asn Thr Val Val Ala Pro Ala Asp Ala Thr Val Ile Leu
                570                 575                 580

gtc cag aaa tct gga cac gca gtg gca ttg cgc tta gat agc gga gtt
1891
Val Gln Lys Ser Gly His Ala Val Ala Leu Arg Leu Asp Ser Gly Val
            585                 590                 595

gaa atc ctt gtc cac gtt gga ttg gac acc gtg caa ttg ggc ggc gaa
1939
Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly Glu
        600                 605                 610

ggc ttc acc gtt cac gtt gag cgc agg cag caa gtc aag gcg ggg gat
1987
Gly Phe Thr Val His Val Glu Arg Arg Gln Gln Val Lys Ala Gly Asp
    615                 620                 625
```

```
cca ctg atc act ttt gac gct gac ttc att cga tcc aag gat cta cct
2035
Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg Ser Lys Asp Leu Pro
630                 635                 640                 645

ttg atc acc cca gtt gtg gtg tct aac gcc gcg aaa ttc ggt gaa att
2083
Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu Ile
                650                 655                 660

gaa ggt att cct gca gat cag gca aat tct tcc acg act gtg atc aag
2131
Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile Lys
            665                 670                 675

gtc aac ggc aag aac gag taacctggga tccatgttgc gca
2172
Val Asn Gly Lys Asn Glu
        680


<210> 30
<211> 683
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Met Ala Ser Lys Leu Thr Thr Thr Ser Gln His Ile Leu Glu Asn Leu
  1               5                  10                  15

Gly Gly Pro Asp Asn Ile Thr Ser Met Thr His Cys Ala Thr Arg Leu
             20                  25                  30

Arg Phe Gln Val Lys Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp
         35                  40                  45

Ser Asp Pro Ser Val Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met
     50                  55                  60

Gln Val Val Met Gly Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu
 65                  70                  75                  80

Lys Leu Asp Gly Met Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser
                 85                  90                  95

Ser Ser Lys Lys Glu Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile
            100                 105                 110

Asp Tyr Ala Phe Glu Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp
        115                 120                 125

Ala Leu Leu Gly Ala Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp
    130                 135                 140

Thr Phe Gly Leu Gln Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp
145                 150                 155                 160

Thr Tyr Val Phe Leu His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu
                165                 170                 175

Pro Ile Met Val Gly Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu
```

```
                180                 185                 190

Trp Ile Gly Ala Ala Ile Pro Ala Ala Leu Leu Thr Pro Glu Phe Leu
        195                 200                 205

Ala Leu Gly Ser Ala Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met
    210                 215                 220

Val Leu Asn Asp Tyr Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala
225                 230                 235                 240

Ile Gly Leu Tyr Trp Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu
                245                 250                 255

Ala Val Gln Met Val Phe Val Pro Phe Phe Ser Leu Leu Ile Met Ile
            260                 265                 270

Pro Ala Thr Ala Phe Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn
        275                 280                 285

Gly Ile Ser Asn Leu Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile
    290                 295                 300

Leu Ser Ile Val Ile Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly
305                 310                 315                 320

Leu His Trp Pro Leu Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu
                325                 330                 335

Gly Tyr Asp Phe Ile Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys
            340                 345                 350

Phe Gly Leu Val Thr Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn
        355                 360                 365

Lys Ala Met Arg Gln Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu
    370                 375                 380

Gly Gly Ile Ser Glu Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys
385                 390                 395                 400

Lys Thr Tyr Phe Arg Leu Leu Pro Gly Cys Leu Ala Gly Gly Ile Val
                405                 410                 415

Met Gly Ile Phe Asp Ile Lys Ala Tyr Ala Phe Val Phe Thr Ser Leu
            420                 425                 430

Leu Thr Ile Pro Ala Met Asp Pro Trp Leu Gly Tyr Thr Ile Gly Ile
        435                 440                 445

Ala Val Ala Phe Phe Val Ser Met Phe Leu Val Leu Ala Leu Asp Tyr
    450                 455                 460

Arg Ser Asn Glu Glu Arg Asp Glu Ala Arg Ala Lys Val Ala Ala Asp
465                 470                 475                 480

Lys Gln Ala Glu Glu Asp Leu Lys Ala Glu Ala Asn Ala Thr Pro Ala
                485                 490                 495

Ala Pro Val Ala Ala Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
            500                 505                 510
```

Ala Ala Gly Ala Ala Thr Ala Val Ala Ala Lys Pro Lys Leu Ala Ala
515 520 525

Gly Glu Val Val Asp Ile Val Ser Pro Leu Glu Gly Lys Ala Ile Pro
530 535 540

Leu Ser Glu Val Pro Asp Pro Ile Phe Ala Ala Gly Lys Leu Gly Pro
545 550 555 560

Gly Ile Ala Ile Gln Pro Thr Gly Asn Thr Val Val Ala Pro Ala Asp
565 570 575

Ala Thr Val Ile Leu Val Gln Lys Ser Gly His Ala Val Ala Leu Arg
580 585 590

Leu Asp Ser Gly Val Glu Ile Leu Val His Val Gly Leu Asp Thr Val
595 600 605

Gln Leu Gly Gly Glu Gly Phe Thr Val His Val Glu Arg Arg Gln Gln
610 615 620

Val Lys Ala Gly Asp Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg
625 630 635 640

Ser Lys Asp Leu Pro Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala
645 650 655

Lys Phe Gly Glu Ile Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser
660 665 670

Thr Thr Val Ile Lys Val Asn Gly Lys Asn Glu
675 680

<210> 31
<211> 1339
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1339)
<223> FRXA02191

<400> 31
ccgattcttt ttcggcccaa ttcgtaacgg cgatcctctt aagtggacaa gaaagtctct 60

tgcccgcggg agacagaccc tacgtttaga aaggtttgac atg gcg tcc aaa ctg 115
Met Ala Ser Lys Leu
1 5

acg acg aca tcg caa cat att ctg gaa aac ctt ggt gga cca gac aat 163
Thr Thr Thr Ser Gln His Ile Leu Glu Asn Leu Gly Gly Pro Asp Asn
10 15 20

att act tcg atg act cac tgt gcg act cgc ctt cgc ttc caa gtg aag 211
Ile Thr Ser Met Thr His Cys Ala Thr Arg Leu Arg Phe Gln Val Lys
25 30 35

gat caa tcc att gtt gat caa caa gaa att gac tcc gac cca tca gtt 259

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Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp Ser Asp Pro Ser Val
          40                  45                  50

ctt ggc gta gta ccc caa gga tcc acc ggt atg cag gtg gtg atg ggt   307
Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met Gln Val Val Met Gly
      55                  60                  65

gga tct gtt gca aac tat tac caa gaa atc ctc aaa ctt gat gga atg   355
Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu Lys Leu Asp Gly Met
 70                  75                  80                  85

aag cac ttc gcc gac ggt gaa gct aca gag agt tca tcc aag aag gaa   403
Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser Ser Ser Lys Lys Glu
                 90                  95                 100

tac ggc gga gtc cgt ggc aag tac tcg tgg att gac tac gcc ttc gag   451
Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile Asp Tyr Ala Phe Glu
            105                 110                 115

ttc ttg tct gat act ttc cga cca atc ctg tgg gcc ctg ctt ggt gcc   499
Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp Ala Leu Leu Gly Ala
        120                 125                 130

tca ctg att att acc ttg ttg gtt ctt gcg gat act ttc ggt ttg caa   547
Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp Thr Phe Gly Leu Gln
    135                 140                 145

gac ttc cgc gct cca atg gat gag cag cct gat act tat gta ttc ctg   595
Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp Thr Tyr Val Phe Leu
150                 155                 160                 165

cac tcc atg tgg cgc tcg gtc ttc tac ttc ctg cca att atg gtt ggt   643
His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu Pro Ile Met Val Gly
                170                 175                 180

gcc acc gca gct cga aag ctc ggc gca aac gag tgg att ggt gca gct   691
Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu Trp Ile Gly Ala Ala
            185                 190                 195

att cca gcc gca ctt ctt act cca gaa ttc ttg gca ctg ggt tct gcc   739
Ile Pro Ala Ala Leu Leu Thr Pro Glu Phe Leu Ala Leu Gly Ser Ala
        200                 205                 210

ggc gat acc gtc aca gtc ttt ggc ctg cca atg gtt ctg aat gac tac   787
Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met Val Leu Asn Asp Tyr
    215                 220                 225

tcc gga cag gta ttc cca ccg ctg att gca gca att ggt ctg tac tgg   835
Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala Ile Gly Leu Tyr Trp
230                 235                 240                 245

gtg gaa aag gga ctg aag aag atc atc cct gaa gca gtc caa atg gtg   883
Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu Ala Val Gln Met Val
                250                 255                 260

ttc gtc cca ttc ttc tcc ctg ctg att atg atc cca gcg acc gca ttc   931
Phe Val Pro Phe Phe Ser Leu Leu Ile Met Ile Pro Ala Thr Ala Phe
            265                 270                 275

ctg ctt gga cct ttc ggc atc ggt gtt ggt aac gga att tcc aac ctg   979
Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn Gly Ile Ser Asn Leu
```

```
        280                 285                 290

ctt gaa gcg att aac aac ttc agc cca ttt att ctt tcc atc gtt atc
1027
Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile Leu Ser Ile Val Ile
    295                 300                 305

cca ttg ctc tac cca ttc ttg gtt cca ctt gga ttg cac tgg cca cta
1075
Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly Leu His Trp Pro Leu
310                 315                 320                 325

aac gcc atc atg atc cag aac atc aac acc ctg ggt tac gac ttc att
1123
Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu Gly Tyr Asp Phe Ile
                330                 335                 340

cag gga cca atg ggt gcc tgg aac ttc gcc tgc ttc ggc ctg gtc acc
1171
Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys Phe Gly Leu Val Thr
            345                 350                 355

ggc gtg ttc ttg ctc tcc att aag gaa cga aac aag gcc atg cgt cag
1219
Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn Lys Ala Met Arg Gln
        360                 365                 370

gtt tcc ctg ggt ggc atg ttg gct ggt ttg ctc ggc ggc att tcc gag
1267
Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu Gly Gly Ile Ser Glu
    375                 380                 385

cct tcc ctc tac ggt gtt ctg ctc cga ttc aag aag acc tac ttc cgc
1315
Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys Lys Thr Tyr Phe Arg
390                 395                 400                 405

ctc ctg ccg ggt tgt ttg gca gca
1339
Leu Leu Pro Gly Cys Leu Ala Ala
                410
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<210> 32
<211> 413
<212> PRT
<213> Corynebacterium glutamicum

<400> 32

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Met Ala Ser Lys Leu Thr Thr Thr Ser Gln His Ile Leu Glu Asn Leu
  1               5                  10                  15

Gly Gly Pro Asp Asn Ile Thr Ser Met Thr His Cys Ala Thr Arg Leu
             20                  25                  30

Arg Phe Gln Val Lys Asp Gln Ser Ile Val Asp Gln Gln Glu Ile Asp
         35                  40                  45

Ser Asp Pro Ser Val Leu Gly Val Val Pro Gln Gly Ser Thr Gly Met
     50                  55                  60
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Gln Val Val Met Gly Gly Ser Val Ala Asn Tyr Tyr Gln Glu Ile Leu
65 70 75 80

Lys Leu Asp Gly Met Lys His Phe Ala Asp Gly Glu Ala Thr Glu Ser
85 90 95

Ser Ser Lys Lys Glu Tyr Gly Gly Val Arg Gly Lys Tyr Ser Trp Ile
100 105 110

Asp Tyr Ala Phe Glu Phe Leu Ser Asp Thr Phe Arg Pro Ile Leu Trp
115 120 125

Ala Leu Leu Gly Ala Ser Leu Ile Ile Thr Leu Leu Val Leu Ala Asp
130 135 140

Thr Phe Gly Leu Gln Asp Phe Arg Ala Pro Met Asp Glu Gln Pro Asp
145 150 155 160

Thr Tyr Val Phe Leu His Ser Met Trp Arg Ser Val Phe Tyr Phe Leu
165 170 175

Pro Ile Met Val Gly Ala Thr Ala Ala Arg Lys Leu Gly Ala Asn Glu
180 185 190

Trp Ile Gly Ala Ala Ile Pro Ala Ala Leu Leu Thr Pro Glu Phe Leu
195 200 205

Ala Leu Gly Ser Ala Gly Asp Thr Val Thr Val Phe Gly Leu Pro Met
210 215 220

Val Leu Asn Asp Tyr Ser Gly Gln Val Phe Pro Pro Leu Ile Ala Ala
225 230 235 240

Ile Gly Leu Tyr Trp Val Glu Lys Gly Leu Lys Lys Ile Ile Pro Glu
245 250 255

Ala Val Gln Met Val Phe Val Pro Phe Phe Ser Leu Leu Ile Met Ile
260 265 270

Pro Ala Thr Ala Phe Leu Leu Gly Pro Phe Gly Ile Gly Val Gly Asn
275 280 285

Gly Ile Ser Asn Leu Leu Glu Ala Ile Asn Asn Phe Ser Pro Phe Ile
290 295 300

Leu Ser Ile Val Ile Pro Leu Leu Tyr Pro Phe Leu Val Pro Leu Gly
305 310 315 320

Leu His Trp Pro Leu Asn Ala Ile Met Ile Gln Asn Ile Asn Thr Leu
325 330 335

Gly Tyr Asp Phe Ile Gln Gly Pro Met Gly Ala Trp Asn Phe Ala Cys
340 345 350

Phe Gly Leu Val Thr Gly Val Phe Leu Leu Ser Ile Lys Glu Arg Asn
355 360 365

Lys Ala Met Arg Gln Val Ser Leu Gly Gly Met Leu Ala Gly Leu Leu
370 375 380

Gly Gly Ile Ser Glu Pro Ser Leu Tyr Gly Val Leu Leu Arg Phe Lys

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Lys Thr Tyr Phe Arg Leu Leu Pro Gly Cys Leu Ala Ala
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  1               5                  10                  15

caa cca act gga aac acc gtt gtt gct cca gca gac gct act gtc atc   96
Gln Pro Thr Gly Asn Thr Val Val Ala Pro Ala Asp Ala Thr Val Ile
             20                  25                  30

ctt gtc cag aaa tct gga cac gca gtg gca ttg cgc tta gat agc gga   144
Leu Val Gln Lys Ser Gly His Ala Val Ala Leu Arg Leu Asp Ser Gly
         35                  40                  45

gtt gaa atc ctt gtc cac gtt gga ttg gac acc gtg caa ttg ggc ggc   192
Val Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly
     50                  55                  60

gaa ggc ttc acc gtt cac gtt gag cgc agg cag caa gtc aag gcg ggg   240
Glu Gly Phe Thr Val His Val Glu Arg Arg Gln Gln Val Lys Ala Gly
 65                  70                  75                  80

gat cca ctg atc act ttt gac gct gac ttc att cga tcc aag gat cta   288
Asp Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg Ser Lys Asp Leu
                85                  90                  95

cct ttg atc acc cca gtt gtg gtg tct aac gcc gcg aaa ttc ggt gaa   336
Pro Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu
            100                 105                 110

att gaa ggt att cct gca gat cag gca aat tct tcc acg act gtg atc   384
Ile Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile
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aag gtc aac ggc aag aac gag taacctggga tccatgttgc gca             428
Lys Val Asn Gly Lys Asn Glu
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  1               5                  10                  15

Gln Pro Thr Gly Asn Thr Val Val Ala Pro Ala Asp Ala Thr Val Ile
            20                  25                  30

Leu Val Gln Lys Ser Gly His Ala Val Ala Leu Arg Leu Asp Ser Gly
        35                  40                  45

Val Glu Ile Leu Val His Val Gly Leu Asp Thr Val Gln Leu Gly Gly
    50                  55                  60

Glu Gly Phe Thr Val His Val Glu Arg Arg Gln Gln Val Lys Ala Gly
65                  70                  75                  80

Asp Pro Leu Ile Thr Phe Asp Ala Asp Phe Ile Arg Ser Lys Asp Leu
                85                  90                  95

Pro Leu Ile Thr Pro Val Val Val Ser Asn Ala Ala Lys Phe Gly Glu
            100                 105                 110

Ile Glu Gly Ile Pro Ala Asp Gln Ala Asn Ser Ser Thr Thr Val Ile
        115                 120                 125

Lys Val Asn Gly Lys Asn Glu
    130                 135
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